

-230-

```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Ala Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 193

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 438 GCG

&lt;400&gt; 193

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

```

-231-

```

      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      320      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      400      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Ala Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      480      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      560      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 194

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 438 GCG

&lt;400&gt; 194

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45

```

-232-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Ala Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 195

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 438 GCG

&lt;400&gt; 195

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

50						55					60				
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr	Asn 170	Met	Glu	Gln	Tyr 175	Leu
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn
Pro	Asn 210	Ser	Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr
Met 225	Glu	Leu	Val	Gly 230	Trp	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys
Ile	Met	Ser 275	Leu	Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285	Gly	Gln	Gln
Pro	Val 290	Glu	Asp	Ile	Ser	Ser 295	Asn	Arg	Ile	Tyr	Lys 300	Ile	Leu	Glu	Leu
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr	Ala	Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	Ala
Thr	Thr	Gly	Lys 340	Thr	Asn	Ile	Ala	Glu 345	Ala	Ile	Ala	His	Thr 350	Val	Pro
Phe	Tyr	Gly 355	Cys	Val	Asn	Trp	Thr	Asn 360	Glu	Asn	Phe	Pro 365	Phe	Asn	Asp
Cys	Val 370	Asp	Lys	Met	Val	Ile 375	Trp	Trp	Glu	Glu	Gly 380	Lys	Met	Thr	Ala
Lys 385	Val	Val	Glu	Ser	Ala 390	Lys	Ala	Ile	Leu	Gly 395	Gly	Ser	Lys	Val	Arg 400
Val	Asp	Gln	Lys	Cys 405	Lys	Ser	Ser	Ala	Gln 410	Ile	Asp	Pro	Thr	Pro 415	Val
Ile	Val	Thr	Ser 420	Asn	Thr	Asn	Met	Cys 425	Ala	Val	Ile	Asp	Gly 430	Asn	Ser
Thr	Thr	Phe 435	Glu	His	Ala	Gln	Pro 440	Leu	Gln	Asp	Arg	Met 445	Phe	Lys	Phe
Glu	Leu 450	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Lys 460	Val	Thr	Lys	Gln
Glu 465	Val	Lys	Asp	Phe	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu	Val 480
Glu	His	Glu	Phe	Tyr 485	Val	Lys	Lys	Gly	Gly 490	Ala	Lys	Lys	Arg	Pro 495	Ala
Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu 510	Ser	Val
Ala	Gln	Pro 515	Ser	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn	Tyr 525	Ala	Asp
Arg	Leu 530	Ala	Arg	Gly	His	Ser 535	Leu								



-234-

<210> 196  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 438 GCG

<400> 196  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Ala Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 197  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 440 GCG

<400> 197  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

-235-

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

Ala	Gln	Pro	500	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515						520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
545					550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
			565						570						575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600					605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615					620					

```
<220>
<223> Mutant rep protein: rep52 440 GCG .
```

<div><div><div>&lt;400&gt;</div><div>198</div></div></div>																
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
1				5					10					15		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			20					25					30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
	50					55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115				120						125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150				155						160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Ala	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230				235						240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			260					265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		275					280					285				

-237-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 199

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 440 GCG

&lt;400&gt; 199

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

-238-

290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Leu Ala Arg Gly His Ser Leu		525
	530	535

<210> 200  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant -rep protein: rep40 440 GCG

<400> 200
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 55 60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

-239-

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Ala Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 201

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 451 GCC

&lt;400&gt; 201

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

-240-

Ser	Asn	Ser	Arg	245	Gln	Ile	Lys	Ala	250	Ala	Leu	Asp	Asn	Ala	255	Gly	Lys
Ile	Met	Ser	Leu	260	Thr	Lys	Thr	Ala	265	Pro	Asp	Tyr	Leu	Val	270	Gly	Gln
Pro	Val	Glu	Asp	275	Ile	Ser	Ser	280	Asn	Arg	Ile	Tyr	Lys	Ile	285	Leu	Glu
Asn	Gly	Tyr	Asp	290	Pro	Gln	Tyr	295	Ala	Ala	Ser	Val	Phe	Leu	300	Gly	Trp
305	Thr	Lys	Lys	310	Phe	Gly	Lys	315	Arg	Asn	Thr	Ile	Trp	Leu	320	Phe	Gly
Thr	Thr	Gly	Lys	325	Thr	Asn	Ile	330	Ala	Glu	Ala	Ile	Ala	His	335	Thr	Val
Phe	Tyr	Gly	Cys	340	Val	Asn	Trp	345	Thr	Asn	Glu	Asn	Phe	Pro	350	Phe	Asn
Cys	Val	Asp	Lys	355	Met	Val	Ile	360	Trp	Trp	Glu	Glu	Gly	Lys	365	Met	Thr
Lys	Val	Val	Glu	370	Ser	Ala	Lys	375	Ala	Ile	Leu	Gly	Gly	Ser	380	Lys	Val
Val	Asp	Gln	Lys	385	Cys	Lys	Ser	390	Ser	Ala	Gln	Ile	Asp	Pro	395	Thr	Pro
Ile	Val	Thr	Ser	405	Asn	Thr	Asn	410	Met	Cys	Ala	Val	Ile	Asp	415	Gly	Asn
Thr	Thr	Phe	Glu	420	His	Gln	Gln	425	Pro	Leu	Gln	Asp	Arg	Met	430	Phe	Lys
Glu	Leu	Ala	Arg	435	Arg	Leu	Asp	440	His	Asp	Phe	Gly	Lys	Val	445	Thr	Lys
Glu	Val	Lys	Asp	450	Phe	Phe	Arg	455	Trp	Ala	Lys	Asp	His	Val	460	Val	Glu
465	Glu	His	Glu	470	Phe	Tyr	Val	475	Lys	Lys	Gly	Gly	Ala	Lys	480	Lys	Arg
Pro	Ser	Asp	Ala	485	Asp	Ile	Ser	490	Pro	Lys	Arg	Val	Arg	Glu	495	Ser	Val
Ala	Gln	Pro	Ser	500	Thr	Ser	Asp	505	Ala	Glu	Ala	Ser	Ile	Asn	510	Tyr	Ala
Arg	Tyr	Gln	Asn	515	Lys	Cys	Ser	520	Arg	His	Val	Gly	Met	Asn	525	Leu	Met
Phe	Pro	Cys	Arg	530	Gln	Cys	Glu	535	Arg	Met	Asn	Gln	Asn	Ser	540	Asn	Ile
545	Phe	Thr	His	550	Gly	Gln	Lys	555	Asp	Cys	Leu	Glu	Cys	Phe	560	Pro	Val
Ser	Gln	Pro	Val	565	Ser	Val	Val	570	Lys	Ala	Tyr	Gln	Lys	Leu	575	Cys	Tyr
Ile	His	His	Ile	580	Met	Gly	Lys	585	Pro	Asp	Ala	Cys	Thr	Ala	590	Cys	Asp
Leu	Val	Asn	Val	595	Asp	Leu	Asp	600	Cys	Ile	Phe	Glu	Gln		605		
610								615							620		

&lt;210&gt; 202

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 451 GCC

&lt;400&gt; 202

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		

-241-

```

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
   35         40         45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50         55         60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65         70         75         80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
   85         90         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100        105        110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115        120        125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130        135        140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145        150        155        160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165        170        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180        185        190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195        200        205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210        215        220
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225        230        235        240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245        250        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 260        265        270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275        280        285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290        295        300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
 305        310        315        320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
 325        330        335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
 340        345        350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
 355        360        365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370        375        380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 385        390        395

```

&lt;210&gt; 203

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 451 GCC

&lt;400&gt; 203

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1         5         10         15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20        25        30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

```



Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro.	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					3					

-243-

Arg Leu Ala Arg Gly His Ser Leu  
530 535

<210> 204  
<211> 312  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mutant rep protein: rep40 451 GCC

<400> 204  
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
1 5 10 15  
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
20 25 30  
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
35 40 45  
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
50 55 60  
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
65 70 75 80  
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
85 90 95  
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
100 105 110  
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
115 120 125  
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
130 135 140  
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
145 150 155 160  
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
165 170 175  
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
180 185 190  
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
195 200 205  
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
210 215 220  
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
225 230 235 240  
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
245 250 255  
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
260 265 270  
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
275 280 285  
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
290 295 300  
Arg Leu Ala Arg Gly His Ser Leu  
305 310

<210> 205  
<211> 621  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mutant rep protein: rep78 460 GCG

-244-

&lt;400&gt; 205

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130						135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Ala	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480

-245-

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 206

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 460 GCG

&lt;400&gt; 206

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Ala Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

-246-

```

      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 207

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 460 GCG

&lt;400&gt; 207

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270

```

-247-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Ala Val Thr Lys Gln
      450      455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 208

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 460 GCG

&lt;400&gt; 208

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

```

-248-

130		135		140
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu Gly Lys Met Thr Ala			
145		150		155
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly Gly Ser Lys Val Arg			
		165		170
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile Asp Pro Thr Pro Val			
		180		185
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val Ile Asp Gly Asn Ser			
		195		200
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp Arg Met Phe Lys Phe			
		210		215
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly Ala Val Thr Lys Gln			
225		230		235
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp His Val Val Glu Val			
		245		250
Glu His Glu Phe Tyr Val	Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala			
		260		265
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg Val Arg Glu Ser Val			
		275		280
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp			
		290		295
Arg Leu Ala Arg Gly His	Ser Leu			300
305		310		

&lt;210&gt; 209

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 462 GCC

&lt;400&gt; 209

Thr Ala Gly Phe Tyr Glu Ile Val	Ile Lys Val Pro Ser Asp Leu Asp
1	15
Glu His Leu Pro Gly Ile Ser Asp	Ser Phe Val Asn Trp Val Ala Glu
	30
Lys Glu Trp Glu Leu Pro Pro Asp	Ser Asp Met Asp Leu Asn Leu Ile
	45
Glu Gln Ala Pro Leu Thr Val Ala	Glu Lys Leu Gln Arg Asp Phe Leu
50	60
Thr Glu Trp Arg Arg Val Ser Lys	Ala Pro Glu Ala Leu Phe Phe Val
65	80
Gln Phe Glu Lys Gly Glu Ser Tyr	Phe His Met His Val Leu Val Glu
	95
Thr Thr Gly Val Lys Ser Met Val	Leu Gly Arg Phe Leu Ser Gln Ile
	110
Arg Glu Lys Leu Ile Gln Arg Ile	Tyr Arg Gly Ile Glu Pro Thr Leu
	125
Pro Asn Trp Phe Ala Val Thr Lys	Thr Arg Asn Gly Ala Gly Gly Gly
130	140
Asn Lys Val Val Asp Glu Cys Tyr	Ile Pro Asn Tyr Leu Leu Pro Lys
145	160
Thr Gln Pro Glu Leu Gln Trp Ala	Trp Thr Asn Met Glu Gln Tyr Leu
	175
Ser Ala Cys Leu Asn Leu Thr Glu	Arg Lys Arg Leu Val Ala Gln His
	190
Leu Thr His Val Ser Gln Thr Gln	Glu Gln Asn Lys Glu Asn Gln Asn
	205
Pro Asn Ser Asp Ala Pro Val Ile	Arg Ser Lys Thr Ser Ala Arg Tyr
210	220

-249-

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 210

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 462 GCC

&lt;400&gt; 210

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys



-250-

1				5					10				15
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn
			20					25				30	Ala
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala
		35					40					45	Gly
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gln
	50					55					60		Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu
	65				70					75			Glu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly
			85					90					Trp
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly
			100					105					Pro
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr
		115					120				125		Val
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe
	130					135					140		Asn
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met
	145				150				155				Thr
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys
				165					170				Val
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr
		180						185				190	Pro
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly
	195					200					205		Asn
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe
	210				215						220		Lys
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Ala
	225				230				235				Lys
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val
			245					250					Glu
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg
		260						265				270	Pro
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu
	275						280					285	Ser
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr
	290				295						300		Ala
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu
	305				310					315			Met
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn
			325						330				Ile
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val
		340						345				350	Ser
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu
		355				360					365		Cys
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala
	370				375						380		Cys
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln	
	385				390					395			

<210> 211  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 462 GCC

<400> 211  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

-251-

Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
		50				55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210					215				220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290					295				300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370					375				380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Ala	Lys	Gln
		450					455				460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val

-252-

Ala	Gln	Pro	500	Ser	Thr	Ser	Asp	Ala	505	Glu	Ala	Ser	Ile	Asn	510	Tyr	Ala	Asp
		515						520						525				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530						535											

<210> 212  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 462 GCC

<400> 212  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 213  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

-253-

&lt;220&gt;

&lt;223&gt; Mutant rep protein:rep 78 462 ATA

&lt;400&gt; 213

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ile Lys Gln

```

-254-

450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475							480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
				485						490							495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500						505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530						535				540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565						570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	595						600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615						620					

&lt;210&gt; 214

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 462 ATA

&lt;400&gt; 214

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5					10					15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
	35						40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55				60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70				75					80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90						95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150				155					160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180					185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195					200						205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210					215					220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Ile	Lys	Gln		
225					230					235					240		

-255-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 215

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 462 ATA

&lt;400&gt; 215

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

-256-

```

                245                250                255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                260                265                270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                275                280                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                290                295                300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                310                315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                330                335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                340                345                350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                355                360                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370                375                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                390                395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                410                415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420                425                430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435                440                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ile Lys Gln
450                455                460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                470                475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                490                495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500                505                510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515                520                525
Arg Leu Ala Arg Gly His Ser Leu
530                535

```

&lt;210&gt; 216

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 462 ATA

&lt;400&gt; 216

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110

```

-257-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ile Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 217

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 484 GCC

&lt;400&gt; 217

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

```



-258-

195	200	205
Pro Asn Ser Asp Ala	Pro Val Ile Arg Ser Lys Thr	Ser Ala Arg Tyr
210	215	220
Met Glu Leu Val Gly Trp	Leu Val Asp Lys Gly Ile Thr	Ser Glu Lys
225	230	235
Gln Trp Ile Gln Glu Asp	Gln Ala Ser Tyr Ile Ser Phe	Asn Ala Ala
245	250	255
Ser Asn Ser Arg Ser Gln	Ile Lys Ala Ala Leu Asp	Asn Ala Gly Lys
260	265	270
Ile Met Ser Leu Thr Lys	Thr Ala Pro Asp Tyr Leu	Val Gly Gln Gln
275	280	285
Pro Val Glu Asp Ile Ser	Ser Asn Arg Ile Tyr Lys	Ile Leu Glu Leu
290	295	300
Asn Gly Tyr Asp Pro Gln	Tyr Ala Ala Ser Val Phe	Leu Gly Trp Ala
305	310	315
Thr Lys Lys Phe Gly Lys	Arg Asn Thr Ile Trp Leu	Phe Gly Pro Ala
325	330	335
Thr Thr Gly Lys Thr Asn	Ile Ala Glu Ala Ile Ala	His Thr Val Pro
340	345	350
Phe Tyr Gly Cys Val Asn	Trp Thr Asn Glu Asn Phe	Pro Phe Asn Asp
355	360	365
Cys Val Asp Lys Met Val	Ile Trp Trp Glu Glu Gly	Lys Met Thr Ala
370	375	380
Lys Val Val Glu Ser Ala	Lys Ala Ile Leu Gly Gly	Ser Lys Val Arg
385	390	395
Val Asp Gln Lys Cys Lys	Ser Ser Ala Gln Ile Asp	Pro Thr Pro Val
405	410	415
Ile Val Thr Ser Asn Thr	Asn Met Cys Ala Val Ile	Asp Gly Asn Ser
420	425	430
Thr Thr Phe Glu His Gln	Gln Pro Leu Gln Asp Arg	Met Phe Lys Phe
435	440	445
Glu Leu Thr Arg Arg Leu	Asp His Asp Phe Gly Lys	Val Thr Lys Gln
450	455	460
Glu Val Lys Asp Phe Phe	Arg Trp Ala Lys Asp His	Val Val Glu Val
465	470	475
Glu His Glu Ala Tyr Val	Lys Lys Gly Gly Ala Lys	Lys Arg Pro Ala
485	490	495
Pro Ser Asp Ala Asp Ile	Ser Glu Pro Lys Arg Val	Arg Glu Ser Val
500	505	510
Ala Gln Pro Ser Thr Ser	Asp Ala Glu Ala Ser Ile	Asn Tyr Ala Asp
515	520	525
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly Met	Asn Leu Met Leu
530	535	540
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln Asn	Ser Asn Ile Cys
545	550	555
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys Phe	Pro Val Ser Glu
565	570	575
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr Gln	Lys Leu Cys Tyr
580	585	590
Ile His His Ile Met Gly	Lys Val Pro Asp Ala Cys	Thr Ala Cys Asp
595	600	605
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe Glu	Gln
610	615	620

&lt;210&gt; 218

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 484 GCC

-259-

```

<400> 218
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245     250     255
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290     295     300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305     310     315     320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325     330     335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340     345     350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355     360     365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370     375     380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385     390     395

```

&lt;210&gt; 219

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 484 GCC

&lt;400&gt; 219

-260-

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5					10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65				70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
	195						200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275						280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	355						360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390						395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	435						440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465				470						475				480	
Glu	His	Glu	Ala	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala

-261-

				485					490					495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	530					535											

&lt;210&gt; 220

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 484 GCC

&lt;400&gt; 220

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20				25						30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50				55						60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65				70					75					80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90					95				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100				105						110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	145				150					155				160			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
			165					170						175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195						200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	225				230					235				240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245					250						255			
Glu	His	Glu	Ala	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260						265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
	275						280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu										
	305				310												

&lt;210&gt; 221

&lt;211&gt; 621

&lt;212&gt; PRT

-262-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: 78 488 GCG

&lt;400&gt; 221

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185				190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215				220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265				270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295				300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375				380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

-263-

```

      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  465      470      475      480
Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
  545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 222

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 488 GCG

&lt;400&gt; 222

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220

```

-264-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 223

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 488 GCG

&lt;400&gt; 223

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

-265-

```

225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          245          250          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          260          265          270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          275          280          285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
          290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
530          535

```

&lt;210&gt; 224

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 488 GCG

&lt;400&gt; 224

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95

```



-266-

```

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Ala Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

<210> 225  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 495 GCC

```

<400> 225
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

```

-267-

Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		180						185					190		
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
		610					615					620			

&lt;210&gt; 226

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-268-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 495 GCC

&lt;400&gt; 226

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
 260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290     295     300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
 305     310     315     320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
 325     330     335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
 340     345     350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
 355     360     365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
 370     375     380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 385     390     395

```

&lt;210&gt; 227

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-269-

&lt;223&gt; Mutant rep protein: rep68 495 GCC

&lt;400&gt; 227

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65     70     75     80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85     90     95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100    105    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115    120    125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130    135    140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145    150    155    160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165    170    175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180    185    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195    200    205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210    215    220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225    230    235    240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245    250    255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260    265    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275    280    285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290    295    300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305    310    315    320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325    330    335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340    345    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355    360    365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370    375    380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385    390    395    400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405    410    415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420    425    430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435    440    445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450    455    460

```

-270-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 228

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 495 GCC

&lt;400&gt; 228

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

-271-

<210> 229  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 497 GCC

<400> 229  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

-272-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 230

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 497 GCC

&lt;400&gt; 230

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		370				375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

```
<210> 231
<211> 536
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep68 497 GCC

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			



-274-

```

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 232

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 497 GCC

&lt;400&gt; 232

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-275-

65					70					75				80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
				85					90					95
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			100					105					110	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
		115					120					125		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	130				135						140			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
145					150					155				160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
				165					170					175
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
		180						185					190	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
	195						200					205		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	210				215						220			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
225					230					235				240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
				245					250					255
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
		260						265					270	
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
	275						280					285		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	290				295						300			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
305					310									

<210> 233  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 497 CGA

<400> 233														
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu
1				5					10					15
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala
		20						25					30	
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu
	35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe
	50				55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe
65				70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val
		85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln
		100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr
	115				120						125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly
	130				135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro
145				150					155					160

-276-

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 234

&lt;211&gt; 397

-277-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 497 CGA

&lt;400&gt; 234

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390      395

```

&lt;210&gt; 235

&lt;211&gt; 536

&lt;212&gt; PRT

-278-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 497 CGA

&lt;400&gt; 235

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

```

-279-

```

      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 236

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 40 497 CGA

&lt;400&gt; 236

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Arg Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300

```

-280-

Arg Leu Ala Arg Gly His Ser Leu  
305 310

&lt;210&gt; 237

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 78 497 CTC

&lt;400&gt; 237

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5				10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
		180						185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
	195					200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210				215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		260						265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275						280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290				295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	355						360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375				380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg

-281-

```

385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485          490          495
Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595          600          605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
610          615          620

```

&lt;210&gt; 238

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 497 CTC

&lt;400&gt; 238

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175

```



-282-

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395  
  
 <210> 239  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Mutant rep protein: rep68 497 CTC  
  
 <400> 239  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

-283-

```

      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 240

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 497 CTC

&lt;400&gt; 240

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45

```

-284-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Leu Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 241

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 497 TAC

&lt;400&gt; 241

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

```

-285-

130	135	140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		
	165	170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		
	180	185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn		
	195	200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		
	210	215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		
225	230	235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		
	245	250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		
	260	265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		
	275	280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		
	290	295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	485	490
Tyr Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
610	615	620

-286-

<210> 242  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 497 TAC

<400> 242  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Tyr Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 243

-287-

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 497 TAC

&lt;400&gt; 243

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

-288-

```

      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Tyr Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 244

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 497 TAC

&lt;400&gt; 244

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Tyr Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285

```

-289-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 245

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 498 GCT

&lt;400&gt; 245

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala



-290-

370		375		380
Lys Val Val Glu Ser	Ala Lys Ala Ile Leu	Gly Gly Ser Lys Val Arg		
385	390	395		400
Val Asp Gln Lys Cys	Lys Ser Ser Ala Gln	Ile Asp Pro Thr Pro Val		
	405	410		415
Ile Val Thr Ser Asn	Thr Asn Met Cys Ala	Val Ile Asp Gly Asn Ser		
	420	425		430
Thr Thr Phe Glu His	Gln Gln Pro Leu Gln	Asp Arg Met Phe Lys Phe		
	435	440		445
Glu Leu Thr Arg Arg	Leu Asp His Asp Phe	Gly Lys Val Thr Lys Gln		
	450	455		460
Glu Val Lys Asp Phe	Phe Arg Trp Ala Lys	Asp His Val Val Glu Val		
465	470	475		480
Glu His Glu Phe Tyr	Val Lys Lys Gly Gly	Ala Lys Lys Arg Pro Ala		
	485	490		495
Pro Ala Asp Ala Asp	Ile Ser Glu Pro Lys	Arg Val Arg Glu Ser Val		
	500	505		510
Ala Gln Pro Ser Thr	Ser Asp Ala Glu Ala	Ser Ile Asn Tyr Ala Asp		
	515	520		525
Arg Tyr Gln Asn Lys	Cys Ser Arg His Val	Gly Met Asn Leu Met Leu		
	530	535		540
Phe Pro Cys Arg Gln	Cys Glu Arg Met Asn	Gln Asn Ser Asn Ile Cys		
545	550	555		560
Phe Thr His Gly Gln	Lys Asp Cys Leu Glu	Cys Phe Pro Val Ser Glu		
	565	570		575
Ser Gln Pro Val Ser	Val Val Lys Lys	Ala Tyr Gln Lys Leu Cys Tyr		
	580	585		590
Ile His His Ile Met	Gly Lys Val Pro	Asp Ala Cys Thr Ala Cys Asp		
	595	600		605
Leu Val Asn Val Asp	Leu Asp Asp Cys	Ile Phe Glu Gln		
610	615	620		

&lt;210&gt; 246

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 498 GCT

&lt;400&gt; 246

Met Glu Leu Val Gly	Trp Leu Val Asp	Lys Gly Ile Thr Ser	Glu Lys
1	5	10	15
Gln Trp Ile Gln Glu	Asp Gln Ala Ser	Tyr Ile Ser Phe	Asn Ala Ala
	20	25	30
Ser Asn Ser Arg Ser	Gln Ile Lys Ala	Ala Leu Asp Asn	Ala Gly Lys
	35	40	45
Ile Met Ser Leu Thr	Lys Thr Ala Pro	Asp Tyr Leu Val	Gly Gln Gln
	50	55	60
Pro Val Glu Asp Ile	Ser Ser Asn Arg	Ile Tyr Lys Ile	Leu Glu Leu
65	70	75	80
Asn Gly Tyr Asp Pro	Gln Tyr Ala Ala	Ser Val Phe Leu	Gly Trp Ala
	85	90	95
Thr Lys Lys Phe Gly	Lys Arg Asn Thr	Ile Trp Leu Phe	Gly Pro Ala
	100	105	110
Thr Thr Gly Lys Thr	Asn Ile Ala Glu	Ala Ile Ala His	Thr Val Pro
	115	120	125
Phe Tyr Gly Cys Val	Asn Trp Thr	Asn Glu Asn Phe	Pro Phe Asn Asp
	130	135	140
Cys Val Asp Lys Met	Val Ile Trp Trp	Glu Glu Gly Lys	Met Thr Ala
145	150	155	160

-291-

```

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                180                185                190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                195                200                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                210                215                220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225                230                235                240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245                250                255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                260                265                270
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                275                280                285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290                295                300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305                310                315                320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325                330                335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                340                345                350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                355                360                365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370                375                380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385                390                395

```

&lt;210&gt; 247

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 498 GCT

&lt;400&gt; 247

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1                5                10                15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
                20                25                30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
                35                40                45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50                55                60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                70                75                80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85                90                95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
                100                105                110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
                115                120                125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130                135                140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                150                155                160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

```

**-292-**

				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265								
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490					495		
Pro	Ala	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505								

```
<210> 248
<211> 312
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep40 498 GCT
```

```

<400> 248
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10          15
Gln Trp Ile Gln Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20          25          30

```

-293-

```

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 249

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 499 GCC

&lt;400&gt; 249

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

```

-294-

115	120	125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly		
130	135	140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		
165	170	175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		
180	185	190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn		
195	200	205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		
210	215	220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		
225	230	235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		
245	250	255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		
260	265	270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		
275	280	285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		
290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
325	330	335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
340	345	350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
355	360	365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
370	375	380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
405	410	415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
420	425	430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
435	440	445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
450	455	460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
485	490	495
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
500	505	510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
515	520	525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
530	535	540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
565	570	575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
580	585	590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
595	600	605

-295-

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

<210> 250  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 499 GCC

<400> 250  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

-296-

385

390

395

<210> 251  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 499 GCC

&lt;400&gt; 251

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130				135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215						220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290				295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400

-297-

```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                410                415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420                425                430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435                440                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                450                455                460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                470                475                480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                490                495
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                500                505                510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                515                520                525
Arg Leu Ala Arg Gly His Ser Leu
530                535

```

&lt;210&gt; 252

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 499 GCC

&lt;400&gt; 252

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1                5                10                15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                20                25                30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                35                40                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50                55                60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65                70                75                80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                85                90                95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                100                105                110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                115                120                125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130                135                140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                150                155                160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                170                175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                180                185                190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                195                200                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210                215                220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225                230                235                240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245                250                255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

```



-298-

```

      260      265      270
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 253

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 503 GCG

&lt;400&gt; 253

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350

```

-299-

```

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 254

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 503 GCG

&lt;400&gt; 254

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

```

-300-

130		135		140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala				
145		150		155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg				
	165		170	
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Val				
	180		185	
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser				
	195		200	
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe				
	210		215	
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln				
225		230		235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val				
	245		250	
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala				
	260		265	
Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val				
	275		280	
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp				
	290		295	
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu				
305		310		315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys				
	325		330	
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu				
	340		345	
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr				
	355		360	
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp				
	370		375	
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln				
385		390		395

&lt;210&gt; 255

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 503 GCG

&lt;400&gt; 255

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp	
1	5
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	10
	20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	25
	30
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	35
	40
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val	45
	50
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu	55
	60
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile	65
	70
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu	75
	80
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly	85
	90
	95
	100
	105
	110
	115
	120
	125
	130
	135
	140

-301-

```

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 256

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 503 GCG

&lt;400&gt; 256

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

-302-

```

      1           5           10           15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20           25           30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35           40           45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50           55           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65           70           75           80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85           90           95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180          185          190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195          200          205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210          215          220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225          230          235          240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245          250          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260          265          270
Pro Ser Asp Ala Asp Ile Ala Glu Pro Lys Arg Val Arg Glu Ser Val
      275          280          285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290          295          300
Arg Leu Ala Arg Gly His Ser Leu
      305          310

```

&lt;210&gt; 257

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 510 GCA

&lt;400&gt; 257

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
      1           5           10           15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20           25           30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35           40           45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50           55           60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65           70           75           80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85           90           95

```

-303-

Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265				270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290				295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515				520						525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
		530				535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr

-304-

Ile	His	His	580	Ile	Met	Gly	Lys	Val	585	Pro	Asp	Ala	Cys	Thr	590	Ala	Cys	Asp
		595						600						605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln						
	610					615					620							

<210> 258  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 510 GCA

<400> 258

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
		20						25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
	35						40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65				70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145				150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260						265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315				320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
		340						345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			

-305-

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 259

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 510 GCA

&lt;400&gt; 259

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr-Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala



-306-

```

      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
530      535

```

&lt;210&gt; 260

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 510 GCA

&lt;400&gt; 260

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240

```

-307-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 261

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 511 GCA

&lt;400&gt; 261

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
		530				535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555				560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
			595				600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
		610				615					620				

```
<210> 262
<211> 397
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep52 511 GCA
```

<400> 262															
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		

-309-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
    115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
    165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
    180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
    195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
    245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
    260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
    275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
    325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
    340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
    355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
    370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 263

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 511 GCA

&lt;400&gt; 263

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
    20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
    35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
    85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
    100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

```

-310-

Pro	Asn	115	Trp	Phe	Ala	Val	Thr	120	Lys	Thr	Arg	Asn	Gly	125	Ala	Gly	Gly	Gly
	130							135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145				150					155					160				
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
				165					170					175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
			180					185					190					
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
			195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
				245					250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
			275				280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
				325					330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
			485						490					495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val			
			500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 264

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 511 GCA

-311-

<400> 264  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 265  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 512 GCT

<400> 265  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80

-312-

Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105				110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130						135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185				190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265				270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345				350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Ala
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu

-313-

				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 266

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 512 GCT

&lt;400&gt; 266

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
	35						40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170						175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		210				215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Ala
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315				320	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
			325						330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		



-314-

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 267  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 512 GCT

<400> 267  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

-315-

```

          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
   405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
   420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
   485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Ala
   500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   515          520          525
Arg Leu Ala Arg Gly His Ser Leu
530          535

```

&lt;210&gt; 268

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 512 GCT

&lt;400&gt; 268

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
   20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
   35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
   85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
   165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
   180          185          190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195          200          205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210          215          220

```

-316-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Ala  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 269

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 516 GCG

&lt;400&gt; 269

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

-317-

```

305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
          530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
610          615          620

```

&lt;210&gt; 270

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 516 GCG

&lt;400&gt; 270

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95

```

-318-

```

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 271

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 516 GCG

&lt;400&gt; 271

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

```

-319-

Arg	Glu	Lys	100	Leu	Ile	Gln	Arg	Ile	105	Tyr	Arg	Gly	Ile	Glu	110	Pro	Thr	Leu
		115						120						125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly			
		130						135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
			165						170					175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
			180					185					190					
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210						215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			245						250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290						295				300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			325						330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370						375				380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
		420						425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450						455				460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
			485					490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
		500						505					510					
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 272

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-320-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 516 GCG

&lt;400&gt; 272

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 273

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 517 GCT

&lt;400&gt; 273

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

-321-

50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe
65					70					75				80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val
				85					90					95
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln
			100					105					110	
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr
		115					120					125		Leu
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly
						135					140			
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro
145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180				185						190	His
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg
						215					220			Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
				260				265					270	Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280					285		Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
		290				295					300			Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
				340				345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360					365		Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
		370				375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			420				425						430	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
		450				455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
				485					490					Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	Val
Ala	Gln	Pro	Ser	Ala	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515					520					525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu



-322-

```

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
        610          615          620

```

&lt;210&gt; 274

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 517 GCT

&lt;400&gt; 274

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          180          185          190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          195          200          205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210          215          220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225          230          235          240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
          245          250          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          260          265          270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          275          280          285
Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290          295          300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305          310          315          320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

```

-323-

Phe	Thr	His	Gly	325	Gln	Lys	Asp	Cys	Leu	330	Glu	Cys	Phe	Pro	Val	335	Ser	Glu
			340						345							350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr			
		355					360									365		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp			
		370				375						380						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln						
385					390					395								

&lt;210&gt; 275

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 517 GCT

&lt;400&gt; 275

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp			
1				5				10						15				
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu			
		20						25					30					
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile			
		35					40					45						
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu			
		50				55					60							
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val			
65					70					75					80			
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu			
			85					90						95				
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile			
		100						105					110					
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu			
		115					120					125						
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly			
		130				135				140								
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155				160				
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
			165					170						175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
		180						185					190					
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
		210				215				220								
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225				230						235				240				
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			245					250						255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
		260						265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
		290				295				300								
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315				320				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			325					330						335				

-324-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 276

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 517 GCT

&lt;400&gt; 276

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

-325-

```

      195              200              205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210              215              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Ala Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305              310

```

&lt;210&gt; 277

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 517 AAC

&lt;400&gt; 277

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285

```

-326-

```

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
          465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
          530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
          545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
          610          615          620

```

&lt;210&gt; 278

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 517 AAC

&lt;400&gt; 278

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-327-

65	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	80
					85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150						155				160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170						175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
	195						200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
	210				215						220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235					240		
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
				245					250					255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260						265					270				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Asn	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
	290					295					300						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
305					310					315					320		
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
				325					330					335			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
		340						345					350				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		355					360					365					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
	370					375					380						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
385					390					395							

&lt;210&gt; 279

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 517 AAC

&lt;400&gt; 279

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5				10						15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55				60							
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75					80		

-328-

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 280

&lt;211&gt; 312

-329-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 517 AAC

&lt;400&gt; 280

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Asn Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 281

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 518 GCA

&lt;400&gt; 281

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30

```



-330-

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

```
<210> 282
<211> 397
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep52 518 GCA
```

<div><div>&lt;400&gt;</div><div>282</div></div>	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1	Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20						25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		50					55				60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		130				135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185						190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		210				215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
			260					265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
		275					280					285				
Ala	Gln	Pro	Ser	Thr	Ala	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		290				295					300					

-332-

```

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305          310          315          320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
          325          330          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          340          345          350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          355          360          365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385          390          395

```

```

<210> 283
<211> 536
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep68 518 GCA

```

```

<400> 283
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
          35          40          45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
          50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65          70          75          80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
          85          90          95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
          100          105          110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
          115          120          125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
          130          135          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145          150          155          160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
          165          170          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
          180          185          190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
          195          200          205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
          210          215          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          245          250          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          260          265          270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          275          280          285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
          290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

```

-333-

305					310				315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly
				325					330				335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr
			340					345					350
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe
		355					360					365	Asn
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met
	370					375					380		Thr
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys
	385				390					395			Val
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr
			405						410				415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly
		420						425					430
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe
		435					440					445	Lys
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr
	450					455					460		Lys
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val
	465				470					475			Glu
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg
			485					490					495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu
		500						505					510
Ala	Gln	Pro	Ser	Thr	Ala	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr
		515					520					525	Ala
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu						Asp
	530					535							

&lt;210&gt; 284

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 518 GCA

&lt;400&gt; 284

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5				10						15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	65				70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	145				150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	

-334-

```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 285

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 519 GCG

&lt;400&gt; 285

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

```

-335-

```

      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 286

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 519 GCG

&lt;400&gt; 286

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45

```

-336-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65          70          75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180          185          190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195          200          205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210          215          220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225          230          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245          250          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260          265          270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275          280          285
Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290          295          300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305          310          315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325          330          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340          345          350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355          360          365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385          390          395

```

&lt;210&gt; 287

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 519 GCG

&lt;400&gt; 287

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35          40          45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

Thr 65	Glu 65	Trp 65	Arg 65	Arg 65	Val 70	Ser 70	Lys 70	Ala 70	Pro 70	Glu 75	Ala 75	Leu 75	Phe 75	Phe 75	Val 80
Gln 85	Phe 85	Glu 85	Lys 85	Gly 85	Glu 85	Ser 85	Tyr 85	Phe 85	His 90	Met 90	His 90	Val 90	Leu 90	Val 95	Glu 95
Thr 100	Thr 100	Gly 100	Val 100	Lys 100	Ser 100	Met 100	Val 100	Leu 105	Gly 105	Arg 105	Phe 105	Leu 110	Ser 110	Gln 110	Ile 110
Arg 115	Glu 115	Lys 115	Leu 115	Ile 115	Gln 115	Arg 115	Ile 120	Tyr 120	Arg 120	Gly 120	Ile 120	Glu 125	Pro 125	Thr 125	Leu 125
Pro 130	Asn 130	Trp 130	Phe 130	Ala 130	Val 130	Thr 135	Lys 135	Thr 135	Arg 135	Asn 140	Gly 140	Ala 140	Gly 140	Gly 140	Gly 140
Asn 145	Lys 145	Val 145	Val 145	Asp 145	Glu 150	Cys 150	Tyr 150	Ile 150	Pro 155	Asn 155	Tyr 155	Leu 155	Leu 155	Pro 160	Lys 160
Thr 165	Gln 165	Pro 165	Glu 165	Leu 165	Gln 165	Trp 165	Ala 165	Trp 170	Thr 170	Asn 170	Met 170	Glu 170	Gln 170	Tyr 175	Leu 175
Ser 180	Ala 180	Cys 180	Leu 180	Asn 180	Leu 180	Thr 180	Glu 185	Arg 185	Lys 185	Arg 185	Leu 185	Val 185	Ala 190	Gln 190	His 190
Leu 195	Thr 195	His 195	Val 195	Ser 195	Gln 195	Thr 195	Gln 200	Glu 200	Gln 200	Asn 200	Lys 200	Glu 205	Asn 205	Gln 205	Asn 205
Pro 210	Asn 210	Ser 210	Asp 210	Ala 210	Pro 210	Val 215	Ile 215	Arg 215	Ser 215	Lys 215	Thr 220	Ser 220	Ala 220	Arg 220	Tyr 220
Met 225	Glu 225	Leu 225	Val 225	Gly 225	Trp 230	Leu 230	Val 230	Asp 230	Lys 235	Gly 235	Ile 235	Thr 235	Ser 235	Glu 240	Lys 240
Gln 245	Trp 245	Ile 245	Gln 245	Glu 245	Asp 245	Gln 245	Ala 245	Ser 250	Tyr 250	Ile 250	Ser 250	Phe 250	Asn 255	Ala 255	Ala 255
Ser 260	Asn 260	Ser 260	Arg 260	Ser 260	Gln 260	Ile 260	Lys 265	Ala 265	Ala 265	Leu 265	Asp 265	Asn 270	Ala 270	Gly 270	Lys 270
Ile 275	Met 275	Ser 275	Leu 275	Thr 275	Lys 275	Thr 275	Ala 280	Pro 280	Asp 280	Tyr 280	Leu 280	Val 285	Gly 285	Gln 285	Gln 285
Pro 290	Val 290	Glu 290	Asp 290	Ile 290	Ser 290	Ser 295	Asn 295	Arg 295	Ile 295	Tyr 295	Lys 300	Ile 300	Leu 300	Glu 300	Leu 300
Asn 305	Gly 305	Tyr 305	Asp 305	Pro 305	Gln 310	Tyr 310	Ala 310	Ala 310	Ser 310	Val 315	Phe 315	Leu 315	Gly 315	Trp 315	Ala 320
Thr 325	Lys 325	Lys 325	Phe 325	Gly 325	Lys 325	Arg 325	Asn 325	Thr 325	Ile 330	Trp 330	Leu 330	Phe 330	Gly 330	Pro 335	Ala 335
Thr 340	Thr 340	Gly 340	Lys 340	Thr 340	Asn 340	Ile 340	Ala 340	Glu 345	Ala 345	Ile 345	Ala 345	His 345	Thr 350	Val 350	Pro 350
Phe 355	Tyr 355	Gly 355	Cys 355	Val 355	Asn 355	Trp 355	Thr 360	Asn 360	Glu 360	Asn 360	Phe 360	Pro 365	Phe 365	Asn 365	Asp 365
Cys 370	Val 370	Asp 370	Lys 370	Met 370	Val 370	Ile 370	Trp 375	Trp 375	Glu 375	Glu 375	Gly 375	Lys 375	Met 375	Thr 375	Ala 375
Lys 385	Val 385	Val 385	Glu 385	Ser 385	Ala 385	Lys 385	Ala 385	Ile 385	Leu 385	Gly 385	Gly 385	Ser 385	Lys 385	Val 385	Arg 385
Val 390	Asp 390	Gln 390	Lys 390	Cys 390	Lys 390	Ser 390	Ser 390	Ala 390	Gln 395	Ile 395	Asp 395	Pro 395	Thr 395	Pro 395	Val 395
Ile 405	Val 405	Thr 405	Ser 405	Asn 405	Thr 405	Asn 405	Met 405	Cys 410	Ala 410	Val 410	Ile 410	Asp 410	Gly 410	Asn 410	Ser 410
Thr 420	Thr 420	Phe 420	Glu 420	His 420	Gln 420	Gln 420	Pro 425	Leu 425	Gln 425	Asp 425	Arg 425	Met 425	Phe 425	Lys 425	Phe 425
Glu 435	Leu 435	Thr 435													



-338-

<210> 288  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 519 GCG

<400> 288  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Ala Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 289  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 598 GCA

<400> 289  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

-339-

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
                   20                  25                  30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
                   35                  40                  45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
                   50                  55                  60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
                   65                  70                  75                  80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
                   85                  90                  95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
                   100                  105                  110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
                   115                  120                  125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
                   130                  135                  140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
                   145                  150                  155                  160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
                   165                  170                  175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
                   180                  185                  190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
                   195                  200                  205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
                   210                  215                  220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
                   225                  230                  235                  240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   245                  250                  255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   260                  265                  270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   275                  280                  285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   290                  295                  300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   305                  310                  315                  320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   325                  330                  335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   340                  345                  350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                   355                  360                  365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
                   370                  375                  380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                   385                  390                  395                  400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                   405                  410                  415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
                   420                  425                  430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                   435                  440                  445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
                   450                  455                  460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   465                  470                  475                  480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   485                  490                  495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

-340-

Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Ala	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595				600						605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 290

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 598 GCA

&lt;400&gt; 290

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
	35					40						45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115				120						125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195				200						205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210				215						220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260						265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			

-341-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Ala Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 291

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 598 GAC

&lt;400&gt; 291

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

-342-

```

      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Asp Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610      615      620

```

&lt;210&gt; 292

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 598 GAC

&lt;400&gt; 292

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80

```

-343-

```

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360
Ile His His Ile Met Asp Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390      395

```

&lt;210&gt; 293

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 598 AGC

&lt;400&gt; 293

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu

```

-344-

Thr	Thr	Gly	Val	85	Lys	Ser	Met	Val	Leu	90	Gly	Arg	Phe	Leu	95	Ser	Gln	Ile
			100						105						110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu			
		115						120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly			
		130					135				140							
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
				165					170						175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
			180					185					190					
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
		210				215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
				245					250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
		290				295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
				325					330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
		370				375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
				405					410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420				425						430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
		450				455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
		465			470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
				485					490					495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500				505						510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu			
		530				535					540							
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys			
		545			550					555					560			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu			
				565					570						575			

-345-

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Ser Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln  
 610 615 620

<210> 294  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 598 AGC

<400> 294  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr



-346-

```

          355          360          365
Ile His His Ile Met Ser Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385          390          395

```

&lt;210&gt; 295

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 600 GCG

&lt;400&gt; 295

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35          40          45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65          70          75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85          90          95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100          105          110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115          120          125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130          135          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145          150          155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165          170          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180          185          190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195          200          205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210          215          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225          230          235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245          250          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260          265          270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275          280          285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305          310          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355          360          365

```

-347-

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 296

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 600 GCG

&lt;400&gt; 296

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

-348-

```

145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 297

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant -rep protein: rep78 600 CCG

&lt;400&gt; 297

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140      145
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160

```

-349-

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 298

&lt;211&gt; 397

-350-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 600 CCG

&lt;400&gt; 298

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Pro Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 299

&lt;211&gt; 621

&lt;212&gt; PRT

-351-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 601 GCA

&lt;400&gt; 299

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280						285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		340						345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	435					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Ala	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

<220>  
<223> Mutant rep protein: rep52 601 GCA

<400>	300																
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5					10					15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Sér	Arg	Ser	Gln	Ile	Lys	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
		35	-				40				45						
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55					60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
65					70					75					80		
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85						90					95			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105						110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
	130					135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150					155					160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170					175			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			180					185					190				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195					200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		210				215					220						

-353-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Ala Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 301

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 78 335 420 495 GCT GCC GCC

&lt;400&gt; 301

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys



-354-

225					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265					270	
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
			275				280					285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
			290				295				300			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
					310					315				320
305	Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly
					325					330				335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
			355				360					365		
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
			370				375				380			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
					390					395				400
385	Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr
					405					410				415
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			420					425					430	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
			435				440					445		
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
			450				455				460			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
					470					475				480
465	Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg
					485					490				495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
			515				520					525		
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
						535					540			
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
					550					555				560
545	Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val
					565					570				575
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
			580					585					590	
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
			595				600					605		
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
			610			615					620			

&lt;210&gt; 302

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 335 420 495 GCT GCC GCC

&lt;400&gt; 302

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	

-355-

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 303

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 335 420 495 GCT GCC GCC

&lt;400&gt; 303

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu

-356-

Lys	Glu	Trp	20	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35						40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
		50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105						110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
		130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
		210				215						220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
		290				295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355				360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
		370				375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		420					425						430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
		450				455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
465					470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			

-357-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
           515                  520  
 Arg Leu Ala Arg Gly His Ser Leu  
           530                  535

<210> 304  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 335 420 495 GCT GCC GCC

<400> 304  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
           20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
           35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
           50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
   65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
           85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala  
           100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
           115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
           130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
   145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
           165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
           180                  185                  190  
 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
           195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
           210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
   225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
           245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
           260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
           275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
           290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
   305                  310

<210> 305  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>

-358-

&lt;223&gt; Mutant rep protein: rep78 39 140 GCA GCC

&lt;400&gt; 305

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Ala Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460

```

-359-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 306

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 39 140 GCA GCC

&lt;400&gt; 306

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Ala Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

-360-

```

                245                250                255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                260                265                270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                275                280                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                290                295                300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                310                315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                330                335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                340                345                350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                355                360                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370                375                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                390                395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                410                415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420                425                430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435                440                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                450                455                460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                470                475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                490                495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500                505                510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515                520                525
Arg Leu Ala Arg Gly His Ser Leu
530                535

```

&lt;210&gt; 307

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 279 428 451 GCC GCT GCC

&lt;400&gt; 307

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100     105     110

```

-361-

Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Ala	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290				295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ala	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Ala	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455				460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
		530				535				540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp



-362-

595                      600                      605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610                      615                      620

<210> 308  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 279 428 451 GCC GCT  
 GCC

<400> 308  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1                      5                      10                      15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20                      25                      30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35                      40                      45  
 Ile Met Ser Leu Thr Lys Ala Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50                      55                      60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65                      70                      75                      80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85                      90                      95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100                      105                      110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115                      120                      125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130                      135                      140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145                      150                      155                      160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165                      170                      175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180                      185                      190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser  
 195                      200                      205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210                      215                      220  
 Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225                      230                      235                      240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245                      250                      255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260                      265                      270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275                      280                      285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290                      295                      300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305                      310                      315                      320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325                      330                      335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340                      345                      350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355                      360                      365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

-363-

370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 309  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 279 428 451 GCC GCT  
 GCC

<400> 309  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Ala Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

-364-

```

      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
530      535

```

&lt;210&gt; 310

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 279 428 451 GCC GCT GCC

&lt;400&gt; 310

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Ala Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Ala Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240

```

[illegible]

```
<210> 311
<211> 621
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep78 125 237 600 GCG GCC GCG

<400>	311																
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5					10					15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
	50					55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65				70						75					80		
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile		
			100					105					110				
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Ala	Pro	Thr	Leu		
		115					120					125					
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
	130					135					140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys		
145				150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu		
			165						170					175			
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His		
			180					185					190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn		
		195					200					205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr		
	210					215					220						
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Ala	Ser	Glu	Lys		
225				230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			245						250				255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		260					265						270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
		275				280						285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305				310					315					320			

-366-

```

      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

<210> 312  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 125 237 600 GCG GCC GCG

```

<400> 312
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100      105      110

```

-367-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Ala Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 313

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 125 237 600 GCG GCC GCG

&lt;400&gt; 313

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu

```

-368-

```

      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
 130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
 145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
 210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys
 225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 314

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 125 237 600 GCG GCC GCG

-369-

```

<400> 314
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Ala Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

```

<210> 315
<211> 621
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep78 163 259 GCT GCG

```

```

<400> 315
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80

```



-370-

Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145				150						155					160
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165					170						175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245				250						255	
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325					330						335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390						395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410						415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465				470						475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545				550						555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu

-371-

Ser	Gln	Pro	Val	565	Ser	Val	Val	Lys	570	Lys	Ala	Tyr	Gln	Lys	575	Leu	Cys	Tyr
			580						585						590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp			
		595					600								605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln							
	610					615					620							

&lt;210&gt; 316

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 163 259 GCT GCG

&lt;400&gt; 316

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75					80
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		130				135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		210				215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		

-372-

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 317

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 163 259 GCT GCG

&lt;400&gt; 317

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

-373-

```

      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

<210> 318  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 163 259 GCT GCG

```

<400> 318
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220

```

-374-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 319  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 17 127 189 GCG GCT GCG

<400> 319  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

-375-

```

305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          385          390          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          400          405          410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          415          420          425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          430          435          440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          445          450          455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
          460          465          470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          475          480          485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          490          495          500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          505          510          515
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
          520          525          530
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
          535          540          545
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          550          555          560
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          565          570          575
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          580          585          590
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
          595          600          605
          610          615          620

```

&lt;210&gt; 320

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 17 127 189 GCG GCT GCG

&lt;400&gt; 320

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1          5          10          15
Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35          40          45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65          70          75          80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85          90          95

```

-376-

```

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu
      115      120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515      520      525
Arg Leu Ala Arg Gly His Ser Leu
530      535

```

&lt;210&gt; 321

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-377-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 350 428 GCT GCT

&lt;400&gt; 321

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255      260
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
265      270      275
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
280      285      290
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
295      300      305
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

```



-378-

450		455		460
Glu Val Lys Asp Phe	Phe Arg Trp Ala Lys Asp	His Val Val Glu Val		
465	470	475		480
Glu His Glu Phe Tyr	Val Lys Lys Gly Gly Ala Lys Lys Arg Pro			485
	485	490		495
Pro Ser Asp Ala Asp	Ile Ser Glu Pro Lys Arg Val Arg Glu Ser			500
	500	505		510
Ala Gln Pro Ser Thr	Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp			515
	515	520		525
Arg Tyr Gln Asn Lys Cys	Ser Arg His Val Gly Met Asn Leu Met Leu			530
	530	535		540
Phe Pro Cys Arg Gln Cys	Glu Arg Met Asn Gln Asn Ser Asn Ile Cys			545
	545	550		555
Phe Thr His Gly Gln Lys	Asp Cys Leu Glu Cys Phe Pro Val Ser Glu			560
	565	570		575
Ser Gln Pro Val Ser Val	Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr			580
	580	585		590
Ile His His Ile Met Gly	Lys Val Pro Asp Ala Cys Thr Ala Cys Asp			595
	595	600		605
Leu Val Asn Val Asp Leu	Asp Asp Cys Ile Phe Glu Gln			610
	615	620		

&lt;210&gt; 322

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 350 428 GCT GCT

&lt;400&gt; 322

Met Glu Leu Val Gly	Trp Leu Val Asp Lys Gly	Ile Thr Ser Glu Lys
1	5	10
Gln Trp Ile Gln	Glu Asp Gln Ala Ser Tyr	Ile Ser Phe Asn Ala Ala
	20	25
Ser Asn Ser Arg Ser	Gln Ile Lys Ala Ala Leu Asp	Asn Ala Gly Lys
	35	40
Ile Met Ser Leu Thr	Lys Thr Ala Pro Asp Tyr	Leu Val Gly Gln Gln
	50	55
Pro Val Glu Asp Ile	Ser Ser Asn Arg Ile Tyr Lys	Ile Leu Glu Leu
	65	70
Asn Gly Tyr Asp Pro	Gln Tyr Ala Ala Ser Val Phe	Leu Gly Trp Ala
	85	90
Thr Lys Lys Phe Gly	Lys Arg Asn Thr Ile Trp Leu Phe	Gly Pro Ala
	100	105
Thr Thr Gly Lys Thr	Asn Ile Ala Glu Ala Ile Ala His	Ala Val Pro
	115	120
Phe Tyr Gly Cys Val	Asn Trp Thr Asn Glu Asn Phe	Pro Phe Asn Asp
	130	135
Cys Val Asp Lys Met	Val Ile Trp Trp Glu Glu Gly	Lys Met Thr Ala
	145	150
Lys Val Val Glu Ser	Ala Lys Ala Ile Leu Gly Gly	Ser Lys Val Arg
	165	170
Val Asp Gln Lys Cys	Lys Ser Ser Ala Gln Ile Asp	Pro Thr Pro Val
	180	185
Ile Val Thr Ser Asn	Thr Asn Met Cys Ala Val Ala Asp	Gly Asn Ser
	195	200
Thr Thr Phe Glu His	Gln Gln Pro Leu Gln Asp Arg	Met Phe Lys Phe
	210	215
Glu Leu Thr Arg Arg	Leu Asp His Asp Phe Gly	Lys Val Thr Lys Gln
	225	230
		235
		240

-379-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   245                                  250                                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                   260                                  265                                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                                  280                                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                                  295                                  300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305                                  310                                  315                                  320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
                   325                                  330                                  335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                   340                                  345                                  350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                   355                                  360                                  365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370                                  375                                  380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385                                  390                                  395

&lt;210&gt; 323

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 350 428 GCT GCT

&lt;400&gt; 323

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1                  5                                  10                                  15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
                   20                                  25                                  30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
                   35                                  40                                  45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50                                  55                                  60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65                                  70                                  75                                  80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
                   85                                  90                                  95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
                   100                                  105                                  110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
                   115                                  120                                  125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130                                  135                                  140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145                                  150                                  155                                  160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
                   165                                  170                                  175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
                   180                                  185                                  190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
                   195                                  200                                  205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210                                  215                                  220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225                                  230                                  235                                  240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

-380-

Ser	Asn	Ser	Arg	245	Ser	Gln	Ile	Lys	Ala	250	Ala	Leu	Asp	Asn	Ala	255	Gly	Lys
Ile	Met	Ser	Leu	260	Thr	Lys	Thr	Ala	265	Pro	Asp	Tyr	Leu	Val	Gly	270	Gln	Gln
Pro	Val	Glu	Asp	275	Ile	Ser	Ser	Asn	280	Arg	Ile	Tyr	Lys	Ile	Leu	285	Glu	Leu
Asn	Gly	Tyr	Asp	290	Pro	Gln	Tyr	Ala	295	Ala	Ser	Val	Phe	Leu	Gly	300	Trp	Ala
305	Thr	Lys	Lys	310	Phe	Gly	Lys	Arg	315	Asn	Thr	Ile	Trp	Leu	Phe	320	Pro	Ala
Thr	Thr	Gly	Lys	325	Thr	Asn	Ile	Ala	330	Glu	Ala	Ile	Ala	His	Ala	335	Val	Pro
Phe	Tyr	Gly	Cys	340	Val	Asn	Trp	Thr	345	Asn	Glu	Asn	Phe	Pro	Phe	350	Asn	Asp
Cys	Val	Asp	Lys	355	Met	Val	Ile	Trp	360	Trp	Glu	Glu	Gly	Lys	Met	365	Thr	Ala
Lys	Val	Val	Glu	370	Ser	Ala	Lys	Ala	375	Ile	Leu	Gly	Gly	Ser	Lys	380	Val	Arg
385	Val	Asp	Gln	390	Lys	Cys	Lys	Ser	395	Ala	Gln	Ile	Asp	Pro	Thr	400	Pro	Val
Ile	Val	Thr	Ser	405	Asn	Thr	Asn	Met	410	Cys	Ala	Val	Ala	Asp	Gly	415	Asn	Ser
Thr	Thr	Phe	Glu	420	His	Gln	Gln	Pro	425	Leu	Gln	Asp	Arg	Met	Phe	430	Lys	Phe
Glu	Leu	Thr	Arg	435	Arg	Leu	Asp	His	440	Asp	Phe	Gly	Lys	Val	Thr	445	Lys	Gln
Glu	Val	Lys	Asp	450	Phe	Phe	Arg	Trp	455	Ala	Lys	Asp	His	Val	Val	460	Glu	Val
465	Glu	His	Glu	470	Tyr	Val	Lys	Lys	475	Gly	Gly	Ala	Lys	Lys	Arg	480	Pro	Ala
Pro	Ser	Asp	Ala	485	Asp	Ile	Ser	Glu	490	Pro	Lys	Arg	Val	Arg	Glu	495	Ser	Val
Ala	Gln	Pro	Ser	500	Thr	Ser	Asp	Ala	505	Glu	Ala	Ser	Ile	Asn	Tyr	510	Ala	Asp
Arg	Leu	Ala	Arg	515	Gly	His	Ser	Leu	520							525		
530									535									

&lt;210&gt; 324

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 350 428 GCT GCT

&lt;400&gt; 324

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			35				40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
			50			55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		

-381-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 325

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 78 54 338 495 GCC GCC GCC

&lt;400&gt; 325

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

```

-382-

Pro	Asn	195	Ser	Asp	Ala	Pro	Val	200	Ile	Arg	Ser	Lys	Thr	205	Ser	Ala	Arg	Tyr
Met	Glu	210	Leu	Val	Gly	Trp	Leu	215	Val	Asp	Lys	Gly	Ile	220	Thr	Ser	Glu	Lys
225	Gln	Trp	Ile	Gln	Glu	Asp	Gln	230	Ala	Ser	Tyr	Ile	Ser	235	Phe	Asn	Ala	Ala
				245							250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	260	Gly	Lys		
			265											270				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	275	Pro	Asp	Tyr	Leu	Val	280	Gln	Gln		
														285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	290	Arg	Ile	Tyr	Lys	Ile	300	Leu	Glu	Leu	
								295										
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	305	Ala	Ser	Val	Phe	Leu	310	Gly	Trp	Ala	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	315	Thr	Ile	Trp	Leu	Phe	320	Gly	Pro	Ala	
				325										330				
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	335	Glu	Ala	Ile	Ala	His	340	Thr	Val	Pro	
														345				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	350	Asn	Glu	Asn	Phe	Pro	355	Phe	Asn	Asp	
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	360	Trp	Glu	Glu	Gly	Lys	365	Met	Thr	Ala	
														370				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	375	Ile	Leu	Gly	Gly	Ser	380	Lys	Val	Arg	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	385	Ala	Gln	Ile	Asp	Pro	390	Thr	Pro	Val	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	400	Cys	Ala	Val	Ile	Asp	405	Gly	Asn	Ser	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	410	Leu	Gln	Asp	Arg	Met	415	Phe	Lys	Phe	
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	420	Asp	Phe	Gly	Lys	Val	425	Thr	Lys	Gln	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	430	Ala	Lys	Asp	His	Val	435	Val	Glu	Val	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	440	Gly	Gly	Ala	Lys	Lys	445	Arg	Ala	Ala	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	450	Pro	Lys	Arg	Val	Arg	455	Glu	Ser	Val	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	460	Glu	Ala	Ser	Ile	Asn	465	Tyr	Ala	Asp	
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	470	His	Val	Gly	Met	Asn	475	Leu	Met	Leu	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	480	Met	Asn	Gln	Asn	Ser	485	Asn	Ile	Cys	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	490	Leu	Glu	Cys	Phe	Pro	495	Val	Ser	Glu	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	500	Lys	Ala	Tyr	Gln	Lys	505	Leu	Cys	Tyr	
Ile	His	His	Ile	Met	Gly	Lys	Val	510	Pro	Asp	Ala	Cys	Thr	515	Ala	Cys	Asp	
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	520	Cys	Ile	Phe	Glu	Gln	525				

&lt;210&gt; 326

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 54 338 495 GCC GCC GCC

-383-

```

<400> 326
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290     295     300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305     310     315     320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325     330     335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340     345     350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355     360     365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370     375     380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385     390     395

```

&lt;210&gt; 327

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 338 495 GCC GCC GCC

&lt;400&gt; 327

-384-

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
		130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290					295				300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala

-385-

Pro	Ser	Asp	Ala	485	Asp	Ile	Ser	Glu	Pro	490	Lys	Arg	Val	Arg	Glu	495	Ser	Val
			500						505						510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 328

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 54 338 495 GCC GCC GCC

&lt;400&gt; 328

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130				135						140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165						170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
		180						185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245						250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
		260						265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	290					295					300				
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
305					310										

&lt;210&gt; 329

&lt;211&gt; 621

&lt;212&gt; PRT



-386-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 350 420 GCT GCC

&lt;400&gt; 329

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90				95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170				175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250				255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330				335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410				415		
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe

-387-

```

      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
610      615      620

```

&lt;210&gt; 330

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 350 420 GCT GCC

&lt;400&gt; 330

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220

```

-388-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 331

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 350 420 GCT GCC

&lt;400&gt; 331

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

-389-

```

225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
Arg Leu Ala Arg Gly His Ser Leu
530          535

```

&lt;210&gt; 332

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 350 420 GCT GCC

&lt;400&gt; 332

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85          90          95

```

-390-

```

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
115 120 125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300
Arg Leu Ala Arg Gly His Ser Leu
305 310

```

<210> 333  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 189 197 518 GCG GCG GCA

```

<400> 333
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1 5 10 15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20 25 30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His

```

-391-

Leu	Thr	His	180	Val	Ala	Gln	Thr	Gln	185	Glu	Gln	Asn	Lys	Glu	190	Asn	Gln	Asn
		195						200						205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225				230						235				240				
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			245						250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
		260						265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
	275						280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305				310						315				320				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			325						330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
		340						345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
	355					360					365							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385				390						395				400				
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
		420						425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
	435						440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465				470						475				480				
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
			485						490					495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
		500						505					510					
Ala	Gln	Pro	Ser	Thr	Ala	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
	515					520						525						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu			
	530					535					540							
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys			
545				550						555				560				
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu			
			565						570					575				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr			
		580						585					590					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp			
	595					600						605						
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln							
	610					615					620							

&lt;210&gt; 334

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-392-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 189 197 518 GCG GCG GCA

&lt;400&gt; 334

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 335

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-393-

&lt;223&gt; Mutant rep protein: rep68 189 197 518 GCG GCG GCA

&lt;400&gt; 335

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His
      180      185      190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255      260
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460

```



-394-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

<210> 336  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 189 197 518 GCG GCG GCA

<400> 336  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ala Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

-395-

<210> 337  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 468 516 GCC GCG

<400> 337  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

-396-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 338

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 468 516 GCC GCG

&lt;400&gt; 338

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

			195				200				205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Ala	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		370				375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

```
<210> 339
<211> 536
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep68 468 516 GCC GCG

[illegible]

-398-

```

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 340

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 468 516 GCC GCG

&lt;400&gt; 340

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-399-

```

65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Ala Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 341

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant-rep protein: rep78 127 221 350 54 140 GCT

GCA GCT GCC GCC

&lt;400&gt; 341

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

```

-400-

145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180					185					190	His
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Arg	Tyr
	210					215					220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265					270	Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
	275						280					285		Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			325						330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Ala	Val
			340					345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	355						360				365			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375				380				Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			405						410					415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420						425					430	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	435						440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455				460				Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485						490					495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
		500						505					510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515						520					525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
545					550					555				Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
			565						570					575
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
	580							585					590	Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
	595						600					605		Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
	610					615					620			

&lt;210&gt; 342

-401-

<211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 127 221 350 54 140 GCT  
 GCA GCT GCC GCC

<400> 342  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 343



-402-

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 127 221 350 54 140 GCT

GCA GCT GCC GCC

&lt;400&gt; 343

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415

```

-403-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

```

<210> 344
<211> 312
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein rep40 127 221 350 54 140 GCT
      GCA GCT GCC GCC

```

```

<400> 344
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270

```

-404-

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   290                  295                  300  
 Arg Leu Ala Arg Gly His Ser Leu  
                   305                  310

<210> 345  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 221 285 GCA GCG

<400> 345  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
   1                  5                  10                  15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
                   20                  25                  30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
                   35                  40                  45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
                   50                  55                  60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
   65                  70                  75                  80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
                   85                  90                  95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
                   100                  105                  110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
                   115                  120                  125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
                   130                  135                  140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
   145                  150                  155                  160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
                   165                  170                  175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
                   180                  185                  190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
                   195                  200                  205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr  
                   210                  215                  220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   225                  230                  235                  240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   245                  250                  255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   260                  265                  270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln  
                   275                  280                  285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
                   290                  295                  300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
   305                  310                  315                  320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   325                  330                  335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   340                  345                  350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

-405-

Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
355	370					375				380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
				420				425					430	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
	465				470					475				480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490						495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515					520					525		
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
	545				550					555				560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
			565					570						575
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
			580					585					590	
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
		595					600					605		
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620			

&lt;210&gt; 346

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 221 285 GCA GCG

&lt;400&gt; 346

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Ala	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	65				70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				

-406-

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 347

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 285 GCA GCG

&lt;400&gt; 347

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

-407-

145	Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
					165					170						175
	Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
				180					185							190
	Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
			195					200					205			
	Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr
		210					215					220				
	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
		225				230					235					240
	Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
					245					250						255
	Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260						265					270		
	Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Ala	Gly	Gln	Gln
			275					280					285			
	Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290					295					300				
	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
		305				310					315					320
	Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325						330					335	
	Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340						345					350		
	Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
			355					360					365			
	Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370					375					380				
	Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
		385				390					395					400
	Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405						410					415	
	Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420						425					430		
	Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
			435					440					445			
	Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450					455					460				
	Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
		465				470					475					480
	Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485						490					495	
	Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500						505					510		
	Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
			515					520					525			
	Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
		530					535									

&lt;210&gt; 348

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 285 GCA GCG

&lt;400&gt; 348

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	

-408-

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Ala Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 349

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 23 495 GCT GCC

&lt;400&gt; 349

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ala Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

			100					105				110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250				255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330				335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450													



-410-

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
           595                  600                  605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
       610                  615                  620

&lt;210&gt; 350

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 23 495 GCT GCC

&lt;400&gt; 350

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1          5          10          15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
           20          25          30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
       35          40          45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
       50          55          60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
       65          70          75          80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
           85          90          95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
          100         105         110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
          115         120         125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
      130         135         140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
      145         150         155         160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
          165         170         175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
          180         185         190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
          195         200         205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
      210         215         220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
      225         230         235         240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
          245         250         255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
          260         265         270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
          275         280         285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
      290         295         300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
      305         310         315         320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
          325         330         335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
          340         345         350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
          355         360         365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

-411-

370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 351  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 23 495 GCT GCC

<400> 351  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ala Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380

-412-

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 352

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 23 495 GCT GCC

&lt;400&gt; 352

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val

-413-

```
<210> 353
<211> 621
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep78 20 54 420 495 GCC GCC
GCC GCC
```

[illegible]

-414-

```

          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
          530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545          550          555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
          610          615          620

```

```

<210> 354
<211> 397
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep52 20 54 420 495 GCC GCC
GCC GCC

```

```

<400> 354
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

```

-415-

```

      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

<210> 355  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

```

<220>
<223> Mutant rep protein: rep68 20 54 420 495 GCC GCC
      GCC GCC

```

```

<400> 355
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

```

-416-

Arg	Glu	Lys	100	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130						135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195						200				205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 356

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-417-

&lt;220&gt;

<223> Mutant rep protein: rep40 20 54 420 495 GCC GCC  
GCC GCC

&lt;400&gt; 356

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 357

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep78 412 612 GCG GCG

&lt;400&gt; 357

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45

```



-418-

Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
50						55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
			115					120				125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
						135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
			195					200				205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
					215						220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
				260				265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
			275				280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
					295						300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
				340				345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
				355			360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
				370			375				380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
				420				425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
				435			440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
					455						460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
				500				505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
				515			520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu

-419-

530	535	540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Ala Asp Leu Asp Asp Cys Ile Phe Glu Gln		
610	615	620

&lt;210&gt; 358

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 412 612 GCC GCG

&lt;400&gt; 358

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
	85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	
	100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro	
	115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp	
	130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala	
145	150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg	
	165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val	
	180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser	
	195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe	
	210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln	
225	230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val	
	245
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala	
	260
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val	
	275
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp	
	290
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu	
305	310
	315
	320

Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325					330					335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		370				375					380				
Leu	Val	Asn	Ala	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

```
<210> 359
<211> 536
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep68 412 612 GCC GCG

<div><div>&lt;400&gt;</div><div>359</div></div>	Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1	Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40						45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
		130				135						140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
		210				215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
		290				295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	

-421-

```

          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
          530          535

```

&lt;210&gt; 360

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 412 612 GCC GCG

&lt;400&gt; 360

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          165          170          175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
          180          185          190

```

-422-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

```

<210> 361
<211> 621
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep78 197 412 GCG GCC

```

```

<400> 361
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

```

-423-

Pro	Val	275	Glu	Asp	Ile	Ser	Ser	280	Asn	Arg	Ile	Tyr	Lys	285	Ile	Leu	Glu	Leu
290	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	295	Ala	Ala	Ser	Val	300	Phe	Leu	Gly	Trp	Ala
305	Thr	Lys	Lys	Phe	Gly	Lys	Arg	310	Asn	Thr	Ile	Trp	315	Leu	Phe	Gly	Pro	Ala
				325	Thr	Asn	Ile	330	Ala	Glu	Ala	Ile	335	Ala	His	Thr	Val	Pro
				340	Phe	Tyr	Gly	345	Asn	Trp	Thr	Asn	350	Glu	Asn	Phe	Pro	Phe
				355	Cys	Val	Asn	360	Trp	Trp	Glu	Glu	365	Lys	Met	Thr	Ala	
				370	Cys	Val	Val	375	Glu	Ser	Ala	Lys	380	Ala	Ile	Leu	Gly	Gly
				385	Val	Asp	Gln	390	Lys	Ser	Ser	Ala	395	Gln	Ile	Ala	Pro	Thr
								405	Asn	Thr	Asn	Met	410	Cys	Ala	Val	Ile	Asp
								420	Ser	Asn	Thr	Asn	425	Ala	Val	Ile	Asp	Gly
								430	Thr	Thr	Phe	Glu	435	His	Gln	Gln	Pro	Leu
								440	Gln	Gln	Pro	Leu	445	Gln	Asp	Arg	Met	Phe
								450	Thr	Arg	Arg	Leu	455	His	Asp	Phe	Gly	Lys
								460	Val	Lys	Asp	Phe	465	Val	His	Val	Val	Glu
								470	Glu	Val	Lys	Asp	475	Val	His	Val	Val	Glu
								485	Glu	His	Glu	Phe	490	Tyr	Val	Lys	Lys	Arg
								495	Pro	Ser	Asp	Ala	500	Asp	Ile	Ser	Glu	Pro
								505	Pro	Lys	Arg	Val	510	Arg	Glu	Ser	Val	
								515	Ala	Gln	Pro	Ser	520	Thr	Ser	Asp	Ala	Glu
								525	Ala	Glu	Ala	Ser	530	Ile	Asn	Tyr	Ala	Asp
								535	Arg	Tyr	Gln	Asn	540	Met	Asn	Leu	Met	Leu
								545	Phe	Pro	Cys	Arg	550	Gln	Asn	Ser	Asn	Ile
								555	Phe	Thr	His	Gly	560	Gln	Lys	Asp	Cys	Glu
								565	Ser	Gln	Pro	Val	570	Ser	Val	Val	Lys	Lys
								575	Ile	His	His	Ile	580	Met	Gly	Lys	Val	Pro
								585	Leu	Val	Asp	Leu	590	Asp	Cys	Ala	Cys	Asp
								595	Leu	Val	Asn	Val	600	Thr	Ala	Cys	Asp	
								605	Leu	Val	Asn	Val	610	Glu	Gln			
								615					620					

&lt;210&gt; 362

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 412 GCG GCC

&lt;400&gt; 362

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50						55				60				

-424-

```

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 363

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 412 GCG GCC

&lt;400&gt; 363

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val

```

-425-

65					70					75				80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val
				85					90					95
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln
			100					105					110	
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr
			115				120					125		
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly
	130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro
145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180					185					190	
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg
	210					215					220			
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265					270	
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280					285		
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360				365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	Pro
				405					410					415
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420					425						430	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
				485					490					495
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515					520					525		
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
	530					535								

&lt;210&gt; 364



-426-

<211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 197 412 GCG GCC

<400> 364  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 365  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 412 495 511 GCC GCC GCA

<400> 365  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu

				20					25				30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155				160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165				170						175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235				240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245				250						255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315				320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325				330						335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360									

-428-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                   515                  520                  525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
                   530                  535                  540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545                  550                  555                  560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                   565                  570                  575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                   580                  585                  590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
                   595                  600                  605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
                   610                  615                  620

&lt;210&gt; 366

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 412 495 511 GCC GCC GCA

&lt;400&gt; 366

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                  5                  10                  15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                   20                  25                  30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                   35                  40                  45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                   50                  55                  60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65                  70                  75                  80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                   85                  90                  95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
                   100                  105                  110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                   115                  120                  125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                   130                  135                  140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145                  150                  155                  160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                   165                  170                  175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val  
                   180                  185                  190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
                   195                  200                  205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                   210                  215                  220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225                  230                  235                  240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                   245                  250                  255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
                   260                  265                  270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val  
                   275                  280                  285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

-429-

290	295	300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
305	310	315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
	325	330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	340	345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	355	360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	370	375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
385	390	395

&lt;210&gt; 367

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 412 495 511 GCC GCC GCA

&lt;400&gt; 367

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp		
1	5	10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu		
	20	25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile		
	35	40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu		
	50	55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val		
65	70	75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu		
	85	90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile		
	100	105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu		
	115	120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly		
	130	135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		
	165	170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		
	180	185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn		
	195	200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		
	210	215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		
225	230	235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		
	245	250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		
	260	265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		
	275	280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		
290	295	300

-430-

```

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Ala Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
530          535

```

<210> 368  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 412 495 511 GCC GCC GCA

```

<400> 368
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

```

-431-

Val	Asp	Gln	Lys	165	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Ala	Pro	Thr	175	Pro	Val
			180	Asn	Thr	Asn	Met	Cys	185	Ala	Val	Ile	Asp	Gly	190	Asn	Ser
Ile	Val	Thr	Ser	195	His	Gln	Gln	Pro	200	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
Thr	Thr	Phe	Glu	210	Arg	Arg	Leu	Asp	215	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
Glu	Leu	Thr	Arg	225	230	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	240	Val
Glu	Val	Lys	Asp	245	250	Gly	Ala	Lys	255	Lys	Lys	Arg	Ala	Ala	Val		
Pro	Ser	Asp	Ala	260	Asp	Ile	Ser	Glu	265	Pro	Lys	Arg	Val	Arg	Glu	270	Ala
Ala	Gln	Pro	Ser	275	Thr	Ser	Asp	Ala	280	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
Arg	Leu	Ala	Arg	290	Gly	His	Ser	Leu	295				300				
305							310										

&lt;210&gt; 369

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 98 422 GCC GCC

&lt;400&gt; 369

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
			35				40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
			50				55				60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Ala	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
			115				120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
			130				135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
			195				200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
			210				215				220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	

-432-

```

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 370

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 98 422 GCC GCC

&lt;400&gt; 370

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

```

-433-

```

      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
   85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
  260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
  275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
  305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
  325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
  340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
  355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  385      390      395

```

&lt;210&gt; 371

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 98 422 GCC GCC

&lt;400&gt; 371

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
  35      40      45

```



-434-

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Ala Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu

-435-

530 535

<210> 372  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 98 422 GCC GCC

<400> 372  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Ala Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 373  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 17 127 189 GCG GCT GCG

<400> 373

-436-

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Ala His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Ala Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

-437-

Pro	Ser	Asp	Ala	485	Ile	Ser	Glu	Pro	490	Lys	Arg	Val	Arg	Glu	495	Ser	Val
Ala	Gln	Pro	Ser	500	Thr	Ser	Asp	Ala	505	Glu	Ala	Ser	Ile	Asn	510	Tyr	Ala
Arg	Tyr	Gln	Asn	515	Lys	Cys	Ser	Arg	520	His	Val	Gly	Met	Asn	525	Leu	Met
Phe	Pro	Cys	Arg	530	Gln	Cys	Glu	Arg	535	Met	Asn	Gln	Asn	Ser	540	Asn	Ile
Phe	Thr	His	Gly	545	Gln	Lys	Asp	Cys	550	Leu	Glu	Cys	Phe	Pro	555	Val	Ser
Ser	Gln	Pro	Val	565	Ser	Val	Val	Lys	570	Lys	Ala	Tyr	Gln	Lys	575	Leu	Cys
Ile	His	His	Ile	580	Met	Gly	Lys	Val	585	Pro	Asp	Ala	Cys	Thr	590	Ala	Cys
Leu	Val	Asn	Val	595	Asp	Leu	Asp	Cys	600	Ile	Phe	Glu	Gln		605		
				610					615						620		

&lt;210&gt; 374

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 17 127 189 GCG GCT GCG

&lt;400&gt; 374

Thr	Ala	Gly	Phe	5	Glu	Ile	Val	Ile	10	Lys	Val	Pro	Ser	Asp	15	Leu	Asp
Ala	His	Leu	Pro	20	Gly	Ile	Ser	Asp	25	Ser	Phe	Val	Asn	Trp	30	Val	Ala
Lys	Glu	Trp	Glu	35	Leu	Pro	Pro	Asp	40	Ser	Asp	Met	Asp	Leu	45	Asn	Leu
Glu	Gln	Ala	Pro	50	Leu	Thr	Val	Ala	55	Glu	Lys	Leu	Gln	Arg	60	Asp	Phe
Thr	Glu	Trp	Arg	65	Arg	Val	Ser	Lys	70	Ala	Pro	Glu	Ala	Leu	75	Phe	Val
Gln	Phe	Glu	Lys	85	Gly	Glu	Ser	Tyr	90	Phe	His	Met	His	Val	95	Leu	Val
Thr	Thr	Gly	Val	100	Lys	Ser	Met	Val	105	Leu	Gly	Arg	Phe	Leu	110	Ser	Gln
Arg	Glu	Lys	Leu	115	Ile	Gln	Arg	Ile	120	Tyr	Arg	Gly	Ile	Glu	125	Pro	Ala
Pro	Asn	Trp	Phe	130	Ala	Val	Thr	Lys	135	Thr	Arg	Asn	Gly	Ala	140	Gly	Gly
Asn	Lys	Val	Val	145	Asp	Glu	Cys	Tyr	150	Ile	Pro	Asn	Tyr	Leu	155	Leu	Pro
Thr	Gln	Pro	Glu	165	Leu	Gln	Trp	Ala	170	Trp	Thr	Asn	Met	Glu	175	Gln	Tyr
Ser	Ala	Cys	Leu	180	Asn	Leu	Thr	Glu	185	Arg	Lys	Arg	Leu	Ala	190	Ala	Gln
Leu	Thr	His	Val	195	Ser	Gln	Thr	Gln	200	Glu	Gln	Asn	Lys	Glu	205	Asn	Gln
Pro	Asn	Ser	Asp	210	Ala	Pro	Val	Ile	215	Arg	Ser	Lys	Thr	Ser	220	Ala	Arg
Met	Glu	Leu	Val	225	Gly	Trp	Leu	Val	230	Asp	Lys	Gly	Ile	Thr	235	Ser	Glu
Gln	Trp	Ile	Gln	245	Glu	Asp	Gln	Ala	250	Ser	Tyr	Ile	Ser	Phe	255	Asn	Ala
Ser	Asn	Ser	Arg	260	Ser	Gln	Ile	Lys	265	Ala	Ala	Leu	Asp	Asn	270	Ala	Gly

-438-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 375

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 20 54 495 GCC GCC GCC

&lt;400&gt; 375

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

```

-439-

130	135	140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		160
	165	170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		175
	180	185
Leu Thr His Val Ser Gln Thr Gln Glu Asn Lys Glu Asn Gln Asn		190
	195	200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		205
	210	215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		220
	225	230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		235
	245	250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		255
	260	265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		270
	275	280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		285
	290	295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		300
	305	310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		315
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		335
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		350
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		365
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		380
	385	390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		395
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		415
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		430
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		445
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		460
	465	470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala		475
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		495
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		510
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		525
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		540
	545	550
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		555
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		575
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		590
	595	600
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln		605
	610	615
		620

-440-

<210> 376  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 20 54 495 GCC GCC GCC

<400> 376  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 377

-441-

<211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 20 54 495 GCC GCC GCC

<400> 377  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser



-442-

```

      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 378

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 20 54 495 GCC GCC GCC

&lt;400&gt; 378

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285

```

-443-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 379  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 259 54 GCG GCC

<400> 379  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

-444-

370		375		380
Lys Val Val Glu Ser	Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg			
385	390	395	400	
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val				
	405	410	415	
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser				
	420	425	430	
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe				
	435	440	445	
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln				
	450	455	460	
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val				
465	470	475	480	
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala				
	485	490	495	
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val				
	500	505	510	
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp				
	515	520	525	
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu				
	530	535	540	
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys				
545	550	555	560	
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu				
	565	570	575	
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr				
	580	585	590	
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp				
	595	600	605	
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln				
610	615	620		

&lt;210&gt; 380

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 259 54 GCG GCC

&lt;400&gt; 380

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys				
1	5	10	15	
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala				
	20	25	30	
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys				
	35	40	45	
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln				
	50	55	60	
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu				
65	70	75	80	
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala				
	85	90	95	
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala				
	100	105	110	
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro				
	115	120	125	
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp				
	130	135	140	
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala				
145	150	155	160	

-445-

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 381

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant\_rep protein: rep68 259 54 GCG GCC

&lt;400&gt; 381

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

-446-

```

                165                170                175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
                180                185                190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
                195                200                205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
                210                215                220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
                225                230                235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                250                255
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                260                265                270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                275                280                285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                290                295                300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
                305                310                315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                330                335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                340                345                350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                355                360                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                370                375                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                385                390                395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                410                415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420                425                430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435                440                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                450                455                460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                465                470                475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                490                495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                500                505                510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                515                520                525
Arg Leu Ala Arg Gly His Ser Leu
                530                535

```

&lt;210&gt; 382

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 259 54 GCG GCC

&lt;400&gt; 382

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20          25          30

```

-447-

```

Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
   35         40         45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50         55         60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   65         70         75         80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
   85         90         95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100        105        110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115        120        125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130        135        140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145        150        155        160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165        170        175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180        185        190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195        200        205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210        215        220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225        230        235        240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  245        250        255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
  260        265        270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
  275        280        285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290        295        300
Arg Leu Ala Arg Gly His Ser Leu
  305        310

```

```

<210> 383
<211> 621
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep78 335 399 GCT GCG

```

```

<400> 383
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1         5         10         15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  20        25        30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
  35        40        45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
  50        55        60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
  65        70        75        80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
  85        90        95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
  100       105       110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

```

-448-

Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
130	115					120					125				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Ala	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Ala	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			

-449-

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

<210> 384  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 335 399 GCT GCG

<400> 384  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln



-450-

385

390

395

&lt;210&gt; 385

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 335 399 GCT GCG

&lt;400&gt; 385

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
          35          40          45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65          70          75          80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
          85          90          95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
          100          105          110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
          115          120          125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
          130          135          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145          150          155          160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
          165          170          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
          180          185          190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
          195          200          205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
          210          215          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          245          250          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          260          265          270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          275          280          285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
          290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg
385          390          395          400

```

-451-

```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
              405              410              415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
              420              425              430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
              435              440              445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
              450              455              460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465              470              475              480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
              485              490              495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
              500              505              510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
              515              520              525
Arg Leu Ala Arg Gly His Ser Leu
530              535

```

&lt;210&gt; 386

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 335 399 GCT GCG

&lt;400&gt; 386

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1              5              10              15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
              20              25              30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
              35              40              45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50              55              60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65              70              75              80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
              85              90              95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Ala Ala
              100              105              110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
              115              120              125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130              135              140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145              150              155              160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Ala Arg
              165              170              175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
              180              185              190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195              200              205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210              215              220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225              230              235              240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
              245              250              255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

```

-452-

260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 387

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 221 432 GCA GCA

&lt;400&gt; 387

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350

-453-

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
           355                          360          365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
           370                          375          380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
   385                          390          395  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                           405          410          415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala  
                           420          425  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
           435                          440          445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
           450                          455          460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
   465                          470          475  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                           485          490          495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                           500          505          510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
           515                          520          525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
           530                          535          540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
   545                          550          555  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                           565          570          575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                           580          585          590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
           595                          600          605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
           610                          615          620

&lt;210&gt; 388

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 221 432 GCA GCA

&lt;400&gt; 388

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                          5          10          15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
           20                          25          30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
           35                          40          45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
           50                          55          60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
   65                          70          75          80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
           85                          90          95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
           100                         105         110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
          115                         120         125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

-454-

130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170						175
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ala
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245				250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
		260						265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
290						295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
305					310					315					320
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
				325				330						335	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 389

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 432 GCA GCA

&lt;400&gt; 389

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85				90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				

-455-

```

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ala
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
530      535

```

&lt;210&gt; 390

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 432 GCA GCA

&lt;400&gt; 390

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

[illegible]

```
<210> 391
<211> 621
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep78 259 516 GCG GCG

<400>	391																
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp		
1				5					10					15			
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu		
			20					25					30				
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile		
		35					40					45					
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu		
		50				55					60						
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val		
65					70					75				80			
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu		
				85					90					95			

-457-

Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130						135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ala	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340				345						350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420					425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		500						505					510		
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr



			580					585				590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

```
<220>
<223> Mutant rep protein: rep52 259 516 GCG GCG
```

[illegible]

-459-

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 393  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 259 516 GCG GCG

<400> 393  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

-460-

```

      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
530      535

```

&lt;210&gt; 394

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 259 516 GCG GCG

&lt;400&gt; 394

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ala Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240

```

-461-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 395

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 495 516 GCC GCG

&lt;400&gt; 395

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala

-462-

				325				330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
			340					345					350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355					360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405					410						415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
			420					425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475					480		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ala	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515					520					525					
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
	530					535					540						
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
	545				550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			565					570						575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585					590				
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600					605					
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
	610					615					620						

&lt;210&gt; 396

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 495 516 GCC GCG

&lt;400&gt; 396

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys		
1				5				10						15			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		
			20					25					30				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
		35					40					45					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
	50					55					60						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	65				70					75				80			
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
			85					90					95				
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				

-463-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 397

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 495 516 GCC GCG

&lt;400&gt; 397

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu

```

Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185				190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265				270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His														

```
<210> 398
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep40 495 516 GCC GCG
```

-465-

<400> 398  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ala Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 399

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence .

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 414 14 GCT GCC

&lt;400&gt; 399

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Ala Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80



-466-

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu

-467-

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 565 570 575  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 400

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 414 14 GCT GCC

&lt;400&gt; 400

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350

-468-

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 401

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 414 14 GCT GCC

&lt;400&gt; 401

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Ala Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp

-469-

```

      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 402

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 414 14 GCT GCC

&lt;400&gt; 402

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220

```

-470-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 403

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 74 402 495 GCG GCC GCC

&lt;400&gt; 403

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

-471-

```

305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          385          390          395
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          400          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
          465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
          530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
          545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          595          600          605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
          610          615          620

```

&lt;210&gt; 404

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 74 402 495 GCG GCC GCC

&lt;400&gt; 404

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
          65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95

```

-472-

```

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390      395

```

&lt;210&gt; 405

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 74 402 495 GCG GCC GCC

&lt;400&gt; 405

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Ala Glu Ala Leu Phe Phe Val
      65      70      75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

```

-473-

Arg	Glu	Lys	100	Leu	Ile	Gln	Arg	Ile	105	Tyr	Arg	Gly	Ile	Glu	110	Pro	Thr	Leu
		115						120						125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly			
	130					135						140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
			165						170					175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
		180						185					190					
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
	195						200					205						
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			245						250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
		260						265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
	275						280					285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			325						330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
		340						345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
	355						360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Ala	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
		420						425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
	435						440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala			
			485					490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
		500						505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
	515						520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 406

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



-474-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 74 402 495 GCG GCC GCC

&lt;400&gt; 406

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Ala Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 407

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 228 462 497 GCC GCC GCC

&lt;400&gt; 407

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

-475-

50	55	60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val		
65	70	75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu		80
	85	90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile		95
	100	105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu		110
	115	120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly		125
	130	135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys		140
145	150	155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu		160
	165	170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His		175
	180	185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn		190
	195	200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr		205
	210	215
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys		220
225	230	235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala		240
	245	250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys		255
	260	265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln		270
	275	280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		285
	290	295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		300
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		320
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		335
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		350
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		365
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		380
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		400
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		415
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		430
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln		445
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		460
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		480
	485	490
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		495
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		510
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		525
	530	535
		540

-476-

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 408

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 228 462 497 GCC GCC GCC

&lt;400&gt; 408

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

-477-

```

          325          330          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          340          345          350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          355          360          365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
          385          390          395

```

&lt;210&gt; 409

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 228 462 497 GCC GCC GCC

&lt;400&gt; 409

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65     70     75     80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85     90     95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100    105    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115    120    125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130    135    140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145    150    155    160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165    170    175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180    185    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195    200    205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210    215    220
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225    230    235    240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245    250    255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260    265    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275    280    285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290    295    300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305    310    315    320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325    330    335

```

-478-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 410

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 228 462 497 GCC GCC GCC

&lt;400&gt; 410

```

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

-479-

```

      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Ala Lys Gln
  225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
  305      310

<210> 411
<211> 621
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant rep protein: rep78 290 338 GCG GCC

<400> 411
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285

```

-480-

```

Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290                295                300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305                310                315                320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                330                335
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                340                345                350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                355                360                365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
                370                375                380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385                390                395                400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                410                415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420                425                430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435                440                445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 450                455                460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465                470                475                480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                490                495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                500                505                510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                515                520                525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
 530                535                540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
 545                550                555                560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565                570                575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                580                585                590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
                595                600                605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
 610                615                620

```

&lt;210&gt; 412

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 290 338 GCG GCC

&lt;400&gt; 412

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1                5                10                15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                20                25                30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                35                40                45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50                55                60
Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-481-

65	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	80
					85					90						95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
			100					105					110				
Thr	Ala	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
		115					120					125					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		130				135					140						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
145					150					155					160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
				165					170						175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
		180						185						190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
		195					200					205					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		210				215					220						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
225					230					235					240		
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
			245						250					255			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
		260						265						270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
		275					280					285					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		290				295					300						
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
305					310					315					320		
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
			325						330					335			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
			340					345					350				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
		355					360					365					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		370			375					380							
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln					
385					390				395								

&lt;210&gt; 413

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 290 338 GCG GCC

&lt;400&gt; 413

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1			5						10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35				40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50				55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75					80	



-482-

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 414

&lt;211&gt; 312

-483-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 290 338 GCG GCC

&lt;400&gt; 414

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Ala Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 415

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 140 511 GCC GCA

&lt;400&gt; 415

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30

```

-484-

Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp

Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

```
<210> 416
<211> 397
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep52 140 511 GCC GCA
```

<div><div><div>&lt;400&gt;</div><div>1</div></div><div><div>416</div><div>5</div></div></div>	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	

-486-

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 417

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 140 511 GCC GCA

&lt;400&gt; 417

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala

-487-

305					310					315				320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360					365		Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
	385				390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			405					410						Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			420					425					430	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
	465				470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490						Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala
			500					505					510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515					520						525		Asp
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
	530					535								

&lt;210&gt; 418

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 140 511 GCC GCA

&lt;400&gt; 418

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			35				40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	65				70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	145				150					155				160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	

-488-

```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 419

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 86 378 GCG GCG

&lt;400&gt; 419

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

```

-489-

Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Ala	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 420

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 86 378 GCG GCG

&lt;400&gt; 420

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			



-490-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Ala Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390      395

```

&lt;210&gt; 421

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep 68 86 378 GCG GCG

&lt;400&gt; 421

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

	50						55				60						
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80		
Gln	Phe	Glu	Lys	Gly 85	Ala	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val	Glu 95		
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile		
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu		
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly		
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160		
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu		
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His		
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln	Glu 200	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn		
Pro	Asn 210	Ser	Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr		
Met 225	Glu	Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240		
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala		
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys		
Ile	Met	Ser 275	Leu	Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285	Gly	Gln	Gln		
Pro	Val 290	Glu	Asp	Ile	Ser	Ser 295	Asn	Arg	Ile	Tyr	Lys 300	Ile	Leu	Glu	Leu		
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr	Ala	Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320		
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	Ala		
Thr	Thr	Gly	Lys 340	Thr	Asn	Ile	Ala	Glu 345	Ala	Ile	Ala	His	Thr 350	Val	Pro		
Phe	Tyr	Gly 355	Cys	Val	Asn	Trp	Thr 360	Asn	Glu	Asn	Phe	Pro 365	Phe	Asn	Asp		
Cys	Val 370	Asp	Lys	Met	Val	Ile 375	Trp	Trp	Ala	Glu	Gly 380	Lys	Met	Thr	Ala		
Lys 385	Val	Val	Glu	Ser	Ala 390	Lys	Ala	Ile	Leu	Gly 395	Gly	Ser	Lys	Val	Arg 400		
Val	Asp	Gln	Lys	Cys 405	Lys	Ser	Ser	Ala 410	Gln	Ile	Asp	Pro	Thr	Pro 415	Val		
Ile	Val	Thr	Ser 420	Asn	Thr	Asn	Met	Cys 425	Ala	Val	Ile	Asp	Gly 430	Asn	Ser		
Thr	Thr	Phe 435	Glu	His	Gln	Gln	Pro 440	Leu	Gln	Asp	Arg	Met 445	Phe	Lys	Phe		
Glu	Leu 450	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Lys 460	Val	Thr	Lys	Gln		
Glu 465	Val	Lys	Asp	Phe	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu	Val 480		
Glu	His	Glu	Phe	Tyr 485	Val	Lys	Lys	Gly	Gly 490	Ala	Lys	Lys	Arg	Pro 495	Ala		
Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu 510	Ser	Val		
Ala	Gln	Pro	Ser 515	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn 525	Tyr	Ala	Asp		
Arg	Leu 530	Ala	Arg	Gly	His	Ser 535	Leu										

-492-

<210> 422  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 86 378 GCG GCG

<400> 422  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Ala Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 423  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 54 86 GCC GCG

<400> 423  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

-493-

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

Ala	Gln	Pro	500	Ser	Thr	Ser	Asp	Ala	505	Glu	Ala	Ser	Ile	Asn	510	Tyr	Ala	Asp
		515						520						525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	535	Arg	His	Val	Gly	Met	Asn	540	Leu	Met	Leu	
Phe	Pro	Cys	Arg	Gln	Cys	Glu	550	Arg	Met	Asn	Gln	555	Asn	Ser	Asn	Ile	Cys	
545					550												560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	570	Cys	Phe	Pro	Val	575	Cys	Tyr		
			580					585										
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	590	Cys	Tyr		
			580					585										
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	605	Cys	Asp		
		595					600											
Leu	Val	Asn	Val	Asp	Leu	Asp	615	Cys	Ile	Phe	Glu	Gln						
		610									620							

```
<210> 424
<211> 536
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep68 54 86 GCC GCG

<div><div><div>&lt;400&gt;</div><div>424</div></div></div>	Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1					5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
			20					25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Ala	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105						110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
			115				120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
			130			135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
			195				200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
						215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
			275				280					285				

-495-

```

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305          310          315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385          390          395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465          470          475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
          530          535

```

&lt;210&gt; 425

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 86 GCC GCG

&lt;400&gt; 425

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
          35          40          45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
          50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65          70          75          80
Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu
          85          90          95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
          100          105          110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
          115          120          125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
          130          135          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

```

-496-

145	Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
					165					170						175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185						190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
	225				230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
	305				310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		340						345				350				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
	385				390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		420					425						430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
	450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
	465				470					475					480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
				485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val	
			500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
		515					520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu	
	530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys	
	545				550					555					560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu	
				565					570					575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr	
			580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp	
		595					600					605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln				
	610					615					620					

&lt;210&gt; 426

-497-

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 86 GCC GCG

&lt;400&gt; 426

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Ala Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```



[illegible]

```
<210> 427
<211> 621
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep78 214 495 140 GCG GCC GCC
```

<div><div>&lt;400&gt;</div><div>427</div></div>	Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1					5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	
		20						25					30			
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	
		35					40					45				
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Ala	Gly	Gly	Gly		
	130					135				140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
			165						170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Ala	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Ala	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				

-499-

```

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 428

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 214 495 140 GCG GCC GCC

&lt;400&gt; 428

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-500-

```

65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390      395

```

&lt;210&gt; 429

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 214 495 140 GCG GCC GCC

&lt;400&gt; 429

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80

```

-501-

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Ala Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Ala Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 430

&lt;211&gt; 312

-502-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 214 495 140 GCG GCC GCC

&lt;400&gt; 430

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 431

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 495 511 GCC GCA

&lt;400&gt; 431

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30

```

-503-

Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		420						425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp

Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

<220>  
<223> Mutant rep protein: rep52 495 511 GCC GCA

[illegible]

-505-

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 433

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 495 511 GCC GCA

&lt;400&gt; 433

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala



-506-

```

305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          325          330          335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          340          345          350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          355          360          365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
          370          375          380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
          405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
          420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
          435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
          450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
          485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
          500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
          515          520          525
Arg Leu Ala Arg Gly His Ser Leu
530          535

```

```

<210> 434
<211> 312
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep40 495 511 GCC GCA

```

```

<400> 434
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
          100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
          115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
          130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
          165          170          175

```

-507-

```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 435

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 495 54 GCC GCC

&lt;400&gt; 435

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175      180
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      185      190      195
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

```

Ile	Met	Ser	260	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	270	Gly	Gln	Gln
		275						280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	295	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
		290										300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala		
305					310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala		
				325					330					335			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
				340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355						360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
		370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg		
385					390					395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
				405					410					415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
				420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435						440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
		450					455					460					
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val		
465					470					475				480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Ala	Ala		
				485					490					495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
				500					505					510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515						520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
		530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
				565					570					575			
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
				580					585					590			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	C						

```

<400> 436
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35          40          45

```

-509-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
  260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
  275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
  305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
  325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
  340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
  355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  385      390      395

```

&lt;210&gt; 437

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 495 54 GCC GCC

&lt;400&gt; 437

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
  35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

50						55						60					
Thr 65	Glu	Trp	Arg	Arg	Val 70	Ser	Lys	Ala	Pro	Glu 75	Ala	Leu	Phe	Phe	Val 80		
Gln	Phe	Glu	Lys	Gly 85	Glu	Ser	Tyr	Phe	His 90	Met	His	Val	Leu	Val 95	Glu		
Thr	Thr	Gly	Val 100	Lys	Ser	Met	Val	Leu 105	Gly	Arg	Phe	Leu	Ser 110	Gln	Ile		
Arg	Glu	Lys 115	Leu	Ile	Gln	Arg	Ile 120	Tyr	Arg	Gly	Ile	Glu 125	Pro	Thr	Leu		
Pro	Asn 130	Trp	Phe	Ala	Val	Thr 135	Lys	Thr	Arg	Asn	Gly 140	Ala	Gly	Gly	Gly		
Asn 145	Lys	Val	Val	Asp	Glu 150	Cys	Tyr	Ile	Pro	Asn 155	Tyr	Leu	Leu	Pro	Lys 160		
Thr	Gln	Pro	Glu	Leu 165	Gln	Trp	Ala	Trp	Thr 170	Asn	Met	Glu	Gln	Tyr 175	Leu		
Ser	Ala	Cys	Leu 180	Asn	Leu	Thr	Glu	Arg 185	Lys	Arg	Leu	Val	Ala 190	Gln	His		
Leu	Thr	His 195	Val	Ser	Gln	Thr	Gln 200	Glu	Gln	Asn	Lys	Glu 205	Asn	Gln	Asn		
Pro	Asn 210	Ser	Asp	Ala	Pro	Val 215	Ile	Arg	Ser	Lys	Thr 220	Ser	Ala	Arg	Tyr		
Met 225	Glu	Leu	Val	Gly	Trp 230	Leu	Val	Asp	Lys	Gly 235	Ile	Thr	Ser	Glu	Lys 240		
Gln	Trp	Ile	Gln	Glu 245	Asp	Gln	Ala	Ser	Tyr 250	Ile	Ser	Phe	Asn	Ala 255	Ala		
Ser	Asn	Ser	Arg 260	Ser	Gln	Ile	Lys	Ala 265	Ala	Leu	Asp	Asn	Ala 270	Gly	Lys		
Ile	Met	Ser 275	Leu	Thr	Lys	Thr	Ala 280	Pro	Asp	Tyr	Leu	Val 285	Gly	Gln	Gln		
Pro	Val 290	Glu	Asp	Ile	Ser	Ser	Asn 295	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
Asn 305	Gly	Tyr	Asp	Pro	Gln 310	Tyr	Ala	Ala	Ser	Val 315	Phe	Leu	Gly	Trp	Ala 320		
Thr	Lys	Lys	Phe	Gly 325	Lys	Arg	Asn	Thr	Ile 330	Trp	Leu	Phe	Gly	Pro 335	Ala		
Thr	Thr	Gly	Lys 340	Thr	Asn	Ile	Ala	Glu 345	Ala	Ile	Ala	His	Thr 350	Val	Pro		
Phe	Tyr	Gly 355	Gys	Val	Asn	Trp	Thr	Asn 360	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
Cys	Val 370	Asp	Lys	Met	Val	Ile 375	Trp	Trp	Glu	Glu	Gly 380	Lys	Met	Thr	Ala		
Lys 385	Val	Val	Glu	Ser	Ala 390	Lys	Ala	Ile	Leu	Gly 395	Gly	Ser	Lys	Val	Arg 400		
Val	Asp	Gln	Lys	Cys 405	Lys	Ser	Ser	Ala	Gln 410	Ile	Asp	Pro	Thr	Pro 415	Val		
Ile	Val	Thr	Ser 420	Asn	Thr	Asn	Met	Cys 425	Ala	Val	Ile	Asp	Gly 430	Asn	Ser		
Thr	Thr	Phe 435	Glu	His	Gln	Gln	Pro 440	Leu	Gln	Asp	Arg	Met	Phe 445	Lys	Phe		
Glu	Leu 450	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Lys 460	Val	Thr	Lys	Gln		
Glu 465	Val	Lys	Asp	Phe	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu	Val 480		
Glu	His	Glu	Phe	Tyr 485	Val	Lys	Lys	Gly	Gly 490	Ala	Lys	Lys	Arg	Ala	Ala		
Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu	Ser	Val		
Ala	Gln	Pro	Ser 515	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn	Tyr 525	Ala	Asp		
Arg	Leu 530	Ala	Arg	Gly	His	Ser 535	Leu										

-511-

<210> 438  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 495 54 GCC GCC

<400> 438  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 439  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 197 495 GCG GCC

<400> 439  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

-512-

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

Ala	Gln	Pro	500	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	510	Tyr	Ala	Asp
		515						520					525				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu		
		530					535					540					
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys		
545					550					555					560		
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu		
				565					570						575		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr		
			580					585							590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp		
		595					600						605				
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln						
		610				615				620							

<213> Artificial Sequence

<223> Mutant rep protein: rep52 197 495 GCG GCC

Met 1	Glu	Leu	Val	Gly 5	Trp	Leu	Val	Asp	Lys 10	Gly	Ile	Thr	Ser	Glu 15	Lys
Gln	Trp	Ile	Gln 20	Glu	Asp	Gln	Ala	Ser 25	Tyr	Ile	Ser	Phe	Asn 30	Ala	Ala
Ser	Asn 35	Ser	Arg	Ser	Gln	Ile	Lys 40	Ala	Ala	Leu	Asp	Asn 45	Ala	Gly	Lys
Ile	Met 50	Ser	Leu	Thr	Lys	Thr 55	Ala	Pro	Asp	Tyr	Leu 60	Val	Gly	Gln	Gln
Pro 65	Val	Glu	Asp	Ile	Ser 70	Ser	Asn	Arg	Ile	Tyr 75	Lys	Ile	Leu	Glu 80	Leu
Asn	Gly	Tyr	Asp	Pro 85	Gln	Tyr	Ala	Ala	Ser 90	Val	Phe	Leu	Gly	Trp 95	Ala
Thr	Lys	Lys	Phe 100	Gly	Lys	Arg	Asn	Thr 105	Ile	Trp	Leu	Phe	Gly 110	Pro	Ala
Thr	Thr	Gly 115	Lys	Thr	Asn	Ile	Ala 120	Glu	Ala	Ile	Ala	His 125	Thr	Val	Pro
Phe	Tyr 130	Gly	Cys	Val	Asn 135	Trp	Thr	Asn	Glu	Asn	Phe 140	Pro	Phe	Asn	Asp
Cys 145	Val	Asp	Lys	Met 150	Val	Ile	Trp	Trp	Glu	Glu 155	Gly	Lys	Met	Thr	Ala
Lys	Val	Val	Glu 165	Ser	Ala	Lys	Ala	Ile	Leu 170	Gly	Gly	Ser	Lys	Val 175	Arg
Val	Asp	Gln 180	Lys	Cys	Lys	Ser	Ser 185	Ala	Gln	Ile	Asp	Pro 190	Thr	Pro	Val
Ile	Val 195	Thr	Ser	Asn	Thr	Asn	Met 200	Cys	Ala	Val	Ile	Asp 205	Gly	Asn	Ser
Thr	Thr 210	Phe	Glu	His	Gln	Gln 215	Pro	Leu	Gln	Asp	Arg 220	Met	Phe	Lys	Phe
Glu 225	Leu	Thr	Arg	Arg	Leu 230	Asp	His	Asp	Phe	Gly 235	Lys	Val	Thr	Lys	Gln
Glu	Val	Lys	Asp	Phe 245	Phe	Arg	Trp	Ala	Lys 250	Asp	His	Val	Val	Glu 255	Val
Glu	His	Glu 260	Phe	Tyr	Val	Lys	Lys	Gly 265	Gly	Ala	Lys	Lys	Arg 270	Ala	Ala
Pro	Ser	Asp 275	Ala	Asp	Ile	Ser	Glu 280	Pro	Lys	Arg	Val	Arg 285	Glu	Ser	Val



-514-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 441  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 197 495 GCG GCC

<400> 441  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

-515-

290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Leu Ala Arg Gly His Ser Leu		
530	535	

&lt;210&gt; 442

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 197 495 GCG GCC

&lt;400&gt; 442

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala	
	85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala	
	100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro	
	115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp	
	130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala	
145	150
	155
	160

-516-

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 443

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 261 20 GCC GCC

&lt;400&gt; 443

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

				245					250					255	
Ser	Asn	Ser	Arg	Ala	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290					295				300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360				365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395				400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440				445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
		530				535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555				560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595													

<220>  
<223> Mutant rep protein: rep52 261 20 GCC GCC

```

<400> 444
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1                    5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
    20          25          30

```

-518-

```

Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
   35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
   50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
   65          70          75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
   85          90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
   100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
   115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
   130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
   145          150          155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
   165          170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
   180          185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
   195          200          205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
   210          215          220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
   225          230          235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
   245          250          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
   260          265          270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
   275          280          285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
   290          295          300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
   305          310          315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
   325          330          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
   340          345          350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
   355          360          365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
   370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
   385          390          395

```

&lt;210&gt; 445

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 261 20 GCC GCC

&lt;400&gt; 445

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
   1          5          10
Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
   20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

```

[illegible]

-520-

Arg Leu Ala Arg Gly His Ser Leu  
530 535

<210> 446  
<211> 312  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mutant rep protein: rep40 261 20 GCC GCC

<400> 446  
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
1 5 10 15  
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
20 25 30  
Ser Asn Ser Arg Ala Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
35 40 45  
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
50 55 60  
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
65 70 75 80  
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
85 90 95  
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
100 105 110  
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
115 120 125  
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
130 135 140  
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
145 150 155 160  
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
165 170 175  
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
180 185 190  
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
195 200 205  
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
210 215 220  
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
225 230 235 240  
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
245 250 255  
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
260 265 270  
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
275 280 285  
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
290 295 300  
Arg Leu Ala Arg Gly His Ser Leu  
305 310

<210> 447  
<211> 621  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Mutant rep protein: rep78 54 20 GCC GCC

-521-

<400> 447  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480



-522-

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 448

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 20 GCC GCC

&lt;400&gt; 448

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Ala Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

-523-

Ile	Met	Ser	260	Leu	Thr	Lys	Thr	Ala	265	Pro	Asp	Tyr	Leu	Val	270	Gly	Gln	Gln
Pro	Val	275	Glu	Asp	Ile	Ser	Ser	280	Asn	Arg	Ile	Tyr	Lys	Ile	285	Leu	Glu	Leu
Asn	Gly	290	Tyr	Asp	Pro	Gln	Tyr	295	Ala	Ala	Ser	Val	Phe	Leu	300	Gly	Trp	Ala
305	Thr	Lys	Lys	Phe	Gly	Lys	Arg	310	Asn	Thr	Ile	Trp	Leu	Phe	315	Gly	Pro	Ala
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	325	Glu	Ala	Ile	Ala	His	Thr	330	Val	Pro	
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	340	Asn	Glu	Asn	Phe	Pro	Phe	345	Asn	Asp	
Cys	Val	355	Asp	Lys	Met	Val	Ile	360	Trp	Glu	Glu	Gly	Lys	Met	365	Thr	Ala	
Lys	Val	370	Val	Glu	Ser	Ala	Lys	375	Ala	Ile	Leu	Gly	Gly	Ser	380	Lys	Val	Arg
385	Val	Asp	Gln	Lys	Cys	Lys	Ser	390	Ser	Ala	Gln	Ile	Asp	Pro	395	Thr	Pro	Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	405	Cys	Ala	Val	Ile	Asp	Gly	410	Asn	Ser	
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	420	Leu	Gln	Asp	Arg	Met	Phe	425	Lys	Phe	
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	435	Asp	Phe	Gly	Lys	Val	Thr	440	Lys	Gln	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	445	Ala	Lys	Asp	His	Val	Val	450	Glu	Val	
465	Glu	His	Glu	Phe	Tyr	Val	Lys	455	Gly	Gly	Ala	Lys	Lys	Arg	460	Pro	Ala	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	470	Pro	Lys	Arg	Val	Arg	Glu	475	Ser	Val	
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	485	Glu	Ala	Ser	Ile	Asn	Tyr	490	Ala	Asp	
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu	500							505			
								515							520			
								530							535			

&lt;210&gt; 449

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 197 420 GCG GCC

&lt;400&gt; 449

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5				10						15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
			35				40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
			50			55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
			115				120					125			

-524-

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln

-525-

610

615

620

&lt;210&gt; 450

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 420 GCG GCC

&lt;400&gt; 450

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

-526-

&lt;210&gt; 451

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 420 GCG GCC

&lt;400&gt; 451

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415

```

-527-

Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 452

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 197 420 GCG GCC

&lt;400&gt; 452

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

-528-

```

      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

```

<210> 453
<211> 621
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep78 54 338 495 GCC GCC GCC

```

```

<400> 453
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365

```

-529-

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 454

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 54 338 495 GCC GCC GCC

&lt;400&gt; 454

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala



-530-

```

145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385          390          395

```

&lt;210&gt; 455

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 338 495 GCC GCC GCC

&lt;400&gt; 455

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65     70     75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85     90     95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100    105    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115    120    125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130    135    140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145    150    155    160

```

-531-

```

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330
Thr Ala Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Ala Ala
      485      490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 456

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 54 338 495 GCC GCC GCC

&lt;400&gt; 456

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1           5           10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

```

[illegible]

```
<210> 457
<211> 621
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep78 197 427 GCG GCG

<400> 457															
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		

-533-

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp

-534-

595                      600                      605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610                      615                      620

<210> 458  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 197 427 GCG GCG

<400> 458  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1                      5                      10                      15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20                      25                      30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35                      40                      45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50                      55                      60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65                      70                      75                      80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85                      90                      95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100                      105                      110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115                      120                      125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130                      135                      140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145                      150                      155                      160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165                      170                      175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180                      185                      190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Ala Ile Asp Gly Asn Ser  
 195                      200                      205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210                      215                      220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225                      230                      235                      240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245                      250                      255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260                      265                      270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275                      280                      285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290                      295                      300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305                      310                      315                      320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325                      330                      335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340                      345                      350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355                      360                      365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370                      375                      380

-535-

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 459

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 427 GCG GCG

&lt;400&gt; 459

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

385					390				395					400	
Val	Asp	Gln	Lys	Cys 405	Lys	Ser	Ser	Ala	Gln 410	Ile	Asp	Pro	Thr	Pro 415	Val
Ile	Val	Thr	Ser	Asn 420	Thr	Asn	Met	Cys 425	Ala	Ala	Ile	Asp	Gly 430	Asn	Ser
Thr	Thr	Phe 435	Glu	His	Gln	Gln	Pro 440	Leu	Gln	Asp	Arg	Met 445	Phe	Lys	Phe
Glu	Leu 450	Thr	Arg	Arg	Leu	Asp 455	His	Asp	Phe	Gly	Lys 460	Val	Thr	Lys	Gln
Glu	Val	Lys	Asp	Phe 465	Phe 470	Arg	Trp	Ala	Lys	Asp 475	His	Val	Val	Glu 480	Val
Glu	His	Glu	Phe 485	Tyr	Val	Lys	Lys	Gly 490	Gly	Ala	Lys	Lys	Arg	Pro 495	Ala
Pro	Ser	Asp	Ala 500	Asp	Ile	Ser	Glu	Pro 505	Lys	Arg	Val	Arg	Glu 510	Ser	Val
Ala	Gln	Pro 515	Ser	Thr	Ser	Asp	Ala 520	Glu	Ala	Ser	Ile	Asn 525	Tyr	Ala	Asp
Arg	Leu 530	Ala	Arg	Gly	His	Ser 535	Leu								

```
<210> 460
<211> 312
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep40 197 427 GCG GCG

<div><div>&lt;400&gt;</div><div>460</div></div>	Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1	Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20						25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
		35					40					45				
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
	50					55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
65					70					75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
				85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			100					105					110			
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145				150					155					160		
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			180					185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Ala	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210					215					220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
				245					250					255		

-537-

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 461

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep protein: rep78 54 228 370 387 GCC GCC  
 GCC GCG

&lt;400&gt; 461

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335



-538-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 462

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

```

<223> Mutant rep protein: rep52 54 228 370 387 GCC GCC
GCC GCG

```

&lt;400&gt; 462

```

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110

```

-539-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 463

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

```

<223> Mutant rep protein: rep68 54 228 370 387 GCC GCC
      GCC GCG

```

&lt;400&gt; 463

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110

```

-540-

```

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515      520      525
Arg Leu Ala Arg Gly His Ser Leu
530      535

```

&lt;210&gt; 464

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-541-

<223> Mutant rep protein: rep40 54 228 370 387 GCC GCC  
GCC GCG

<400> 464

```

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
 100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
 115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
 130     135     140
Cys Ala Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 145     150     155     160
Lys Val Ala Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
 180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
 195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
 225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
 260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
 275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
 290     295     300
Arg Leu Ala Arg Gly His Ser Leu
 305     310

```

<210> 465

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant rep protein: rep78 221 289 GCA GCC

<400> 465

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu

```

-542-

50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe
65					70					75				80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val
				85					90					95
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln
			100					105					110	
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr
		115					120					125		Leu
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly
	130					135				140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro
145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
		180						185					190	His
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg
	210					215				220				Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
		260					265					270		Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
	275						280					285		Gln
Ala	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
				325					330					Ala
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	355						360				365			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375				380				Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
				405					410					Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420				425						430		Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	435						440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
				485					490					Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
	500						505						510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515						520					525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu

-543-

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 466

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 221 289 GCA GCC

&lt;400&gt; 466

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Ala Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys

-544-

Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			340					345					350		
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
		355					360					365			
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	370					375					380				
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
385					390					395					

&lt;210&gt; 467

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 289 GCA GCC

&lt;400&gt; 467

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55				60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85						90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155				160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
			165						170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235				240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			245						250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Ala	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315				320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	

-545-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 468

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 289 GCA GCC

&lt;400&gt; 468

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Ala Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```



-546-

```

      195                200                205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
  305      310

```

&lt;210&gt; 469

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 163 GCC GCT

&lt;400&gt; 469

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285

```

-547-

```

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 470

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 163 GCC GCT

&lt;400&gt; 470

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val

```

-548-

65					70					75				80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val
				85					90					95
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln
			100					105					110	Ile
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr
		115					120					125		Leu
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly
	130					135					140			
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro
145					150					155				Lys
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
			165						170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180					185					190	His
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg
	210					215					220			Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
225					230					235				Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
			245						250					255
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
			260					265					270	Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
		275					280					285		Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290					295					300			Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
305					310					315				Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			325						330					335
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
			340					345					350	Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
		355					360					365		Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370					375					380			Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
385					390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			405						410					Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
		420						425					430	Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
		435					440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450					455					460			Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
465					470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485						490					Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
			500					505					510	Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
		515					520					525		Asp
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu							
	530					535								

&lt;210&gt; 471

-549-

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 341 407 420 GCC GCC GCC

&lt;400&gt; 471

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490					495		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555				560	
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

### <213> Artificial Sequence

<223> Mutant rep protein: rep52 341 407 420 GCC GCC GCC

Met 1	Glu	Leu	Val	Gly 5	Trp	Leu	Val	Asp	Lys 10	Gly	Ile	Thr	Ser	Glu 15	Lys
Gln	Trp	Ile	Gln 20	Glu	Asp	Gln	Ala	Ser 25	Tyr	Ile	Ser	Phe	Asn 30	Ala	Ala
Ser	Asn	Ser 35	Arg	Ser	Gln	Ile	Lys 40	Ala	Ala	Leu	Asp	Asn 45	Ala	Gly	Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr 55	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
Pro	Val	Glu	Asp	Ile	Ser 70	Ser	Asn	Arg	Ile	Tyr 75	Lys	Ile	Leu	Glu	Leu 80
Asn	Gly	Tyr	Asp	Pro 85	Gln	Tyr	Ala	Ala	Ser 90	Val	Phe	Leu	Gly	Trp	Ala
Thr	Lys	Lys	Phe 100	Gly	Lys	Arg	Asn	Thr 105	Ile	Trp	Leu	Phe	Gly 110	Pro	Ala
Thr	Thr	Gly 115	Lys	Ala	Asn	Ile	Ala 120	Glu	Ala	Ile	Ala	His 125	Thr	Val	Pro
Phe	Tyr 130	Gly	Cys	Val	Asn 135	Trp	Thr	Asn	Glu	Asn 140	Phe	Pro	Phe	Asn	Asp
Cys	Val	Asp	Lys	Met 150	Val	Ile	Trp	Trp	Glu	Glu 155	Gly	Lys	Met	Thr	Ala 160
Lys	Val	Val	Glu	Ser 165	Ala	Lys	Ala	Ile	Leu 170	Gly	Gly	Ser	Lys	Val	Arg
Val	Asp	Gln	Lys 180	Cys	Lys	Ala	Ser 185	Ala	Gln	Ile	Asp	Pro	Thr 190	Pro	Val
Ile	Val	Thr 195	Ala	Asn	Thr	Asn 200	Met	Cys	Ala	Val	Ile	Asp 205	Gly	Asn	Ser

-551-

```

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
 210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 473

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 341 407 420 GCC GCC GCC

&lt;400&gt; 473

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr

```

-552-

```

      210                      215                      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225                      230                      235                      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245                      250                      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260                      265                      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275                      280                      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290                      295                      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                      310                      315                      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325                      330                      335
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340                      345                      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355                      360                      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370                      375                      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                      390                      395                      400
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
      405                      410                      415
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420                      425                      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435                      440                      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450                      455                      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                      470                      475                      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485                      490                      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500                      505                      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515                      520                      525
Arg Leu Ala Arg Gly His Ser Leu
530                      535

```

&lt;210&gt; 474

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 341 407 420 GCC GCC GCC

&lt;400&gt; 474

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80

```

-553-

```

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Ala Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170
Val Asp Gln Lys Cys Lys Ala Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 475

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant -rep protein: rep78 54 228 GCC GCC

&lt;400&gt; 475

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
  20      25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
  35      40
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
  50      55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
  65      70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
  85      90
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
  100      105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
  115      120
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
  130      135
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
  145      150
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu

```



-554-

Ser	Ala	Cys	Leu	165	Asn	Leu	Thr	Glu	Arg	170	Lys	Arg	Leu	Val	Ala	175	Gln	His
			180						185						190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200						205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
	210					215					220							
Met	Glu	Leu	Ala	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
				245					250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
	275					280						285						
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	290					295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
				325					330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
	355					360					365							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	370					375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
				405					410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
	435						440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	450					455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
				485					490					495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
	515					520					525							
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu			
	530					535					540							
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys			
545					550					555					560			
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu			
				565					570					575				
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr			
			580					585					590					
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp			
	595					600						605						
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln						
	610					615					620							

&lt;210&gt; 476

&lt;211&gt; 397

&lt;212&gt; PRT

-555-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 54 228 GCC GCC

&lt;400&gt; 476

```

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20     25     30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35     40     45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50     55     60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65     70     75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85     90     95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100    105    110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115    120    125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130    135    140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145    150    155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165    170    175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180    185    190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195    200    205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210    215    220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225    230    235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245    250    255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260    265    270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275    280    285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290    295    300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305    310    315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325    330    335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340    345    350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355    360    365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370    375    380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385    390    395

```

&lt;210&gt; 477

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-556-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 228 GCC GCC

&lt;400&gt; 477

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
 85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

```

-557-

```

      450              455              460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465              470              475              480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485              490              495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500              505              510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515              520              525
Arg Leu Ala Arg Gly His Ser Leu
      530              535

```

&lt;210&gt; 478

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 54 228 GCC GCC

&lt;400&gt; 478

```

Met Glu Leu Ala Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

-558-

<210> 479  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 96 125 511 GCA GCG GCA

<400> 479  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Ala  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

-559-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 480

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 96 125 511 GCA GCG GCA

&lt;400&gt; 480

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

-560-

```

      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225      230      235
Glu Val Lys Asp Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
  305      310      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
  385      390      395

```

&lt;210&gt; 481

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 96 125 511 GCA GCG GCA

&lt;400&gt; 481

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Ala
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Ala Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205

```

-561-

```

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ala Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 482

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 96 125 511 GCA GCG GCA

&lt;400&gt; 482

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```



-562-

65	Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
					85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
		115					120					125				
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
	130					135					140					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
145					150					155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
				165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
		180						185					190			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
		195					200					205				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
	210				215						220					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
225					230					235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	
			245					250						255		
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala	
		260						265					270			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ala	Val	
		275					280					285				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp	
	290					295					300					
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu									
305					310											

&lt;210&gt; 483

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 54 163 GCC GCT

&lt;400&gt; 483

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
		20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
	35						40					45			
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50				55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
		100						105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
	115						120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135				140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160

-563-

Thr Gln Ala Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 484

&lt;211&gt; 536

-564-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 54 163 GCC GCT

&lt;400&gt; 484

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp	1	5	10	15
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu	20	25	30	35
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile	40	45	50	55
Glu	Gln	Ala	Pro	Leu	Ala	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	60	65	70	75
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	80	85	90	95
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	100	105	110	115
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	120	125	130	135
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	140	145	150	155
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	160	165	170	175
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	180	185	190	195
Thr	Gln	Ala	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	200	205	210	215
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	220	225	230	235
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	240	245	250	255
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	260	265	270	275
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	280	285	290	295
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	300	305	310	315
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	320	325	330	335
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	340	345	350	355
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	360	365	370	375
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	380	385	390	395
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	400	405	410	415
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	420	425	430	435
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	440	445	450	455
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	460	465	470	475
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	480	485	490	495
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	500	505	510	515
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	520	525	530	535

-565-

```

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 485

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 197 420 GCG GCC

&lt;400&gt; 485

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-566-

290	295	300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
305	310	315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	325	330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	340	345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	355	360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	370	375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
385	390	395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val		
	405	410
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	420	425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	435	440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	450	455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
465	470	475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	485	490
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	500	505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	515	520
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	530	535
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
545	550	555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	565	570
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	580	585
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	595	600
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln		
610	615	620

&lt;210&gt; 486

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 420 GCG GCC

&lt;400&gt; 486

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys	
1	5
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala	
	20
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys	
	35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln	
	50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu	
65	70

-567-

```

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390

```

&lt;210&gt; 487

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 420 GCG GCC

&lt;400&gt; 487

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      75      80

```

				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145				150					155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
			165					170						175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ala	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210				215						220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225				230					235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
			245					250						255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290				295						300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305				310					315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
			325					330						335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385				390						395				400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
			405						410					415		
Ile	Val	Thr	Ala	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420				</									

```
<210> 488
<211> 312
<212> PRT
```

-569-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 197 420 GCG GCC

&lt;400&gt; 488

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ala Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 489

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 334 428 499 GCG GCT GCC

&lt;400&gt; 489

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile

```



[illegible]

-571-

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
           530                          535                          540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545                          550                          555                          560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
                           565                          570                          575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
                           580                          585                          590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
                           595                          600                          605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
           610                          615                          620

&lt;210&gt; 490

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 334 428 499 GCG GCT GCC

&lt;400&gt; 490

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
   1                          5                          10                          15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
                           20                          25                          30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
                           35                          40                          45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
                           50                          55                          60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65                          70                          75                          80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
                           85                          90                          95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala  
                           100                          105                          110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
                           115                          120                          125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
                           130                          135                          140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145                          150                          155                          160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
                           165                          170                          175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
                           180                          185                          190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser  
                           195                          200                          205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
                           210                          215                          220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225                          230                          235                          240  
 Glu Val Lys Asp Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
                           245                          250                          255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
                           260                          265                          270  
 Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
                           275                          280                          285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
                           290                          295                          300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu

-572-

```

305          310          315          320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
          325          330          335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
          340          345          350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
          355          360          365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
          370          375          380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
          385          390          395

```

<210> 491  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 334 428 499 GCG GCT GCC

```

<400> 491
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
          20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
          35          40          45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
          50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
          65          70          75          80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
          85          90          95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
          100          105          110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
          115          120          125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
          130          135          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
          145          150          155          160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
          165          170          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
          180          185          190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
          195          200          205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
          210          215          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
          225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
          245          250          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          260          265          270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
          275          280          285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
          290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
          305          310          315          320

```

-573-

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 492

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 334 428 499 GCG GCT GCC

&lt;400&gt; 492

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Ala Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val

-574-

```

      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ala Asp Gly Asn Ser
      195      200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Ala Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

```

<210> 493
<211> 621
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep78 197 414 GCG GCT

```

```

<400> 493
Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270

```

-575-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310      315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 494

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 197 414 GCG GCT

&lt;400&gt; 494

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln

```

-576-

50	55	60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu		
65	70	75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala		
	85	90
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala		
	100	105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro		
	115	120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp		
	130	135
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala		
	145	150
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg		
	165	170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val		
	180	185
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser		
	195	200
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe		
	210	215
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln		
	225	230
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val		
	245	250
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala		
	260	265
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val		
	275	280
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp		
	290	295
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu		
	305	310
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys		
	325	330
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu		
	340	345
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr		
	355	360
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp		
	370	375
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln		
	385	390
		395

&lt;210&gt; 495

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 197 414 GCG GCT

&lt;400&gt; 495

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp	
1	5
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu	
	20
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile	
	35
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu	
	50
	55
	60

-577-

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ala Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535



-578-

<210> 496  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 197 414 GCG GCT

<400> 496  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Ala Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 497  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 30 54 127 GCG GCC GCT

<400> 497  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15

-579-

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Ala Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Ala Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Ala Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

[illegible]

-581-

```

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515      520      525
Arg Leu Ala Arg Gly His Ser Ser
530      535

```

&lt;210&gt; 499

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 29 260 GCG GCG

&lt;400&gt; 499

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Ala Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys

```

-582-

145					150					155				160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr
				165					170					175
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln
			180					185					190	His
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln
		195					200					205		Asn
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg
	210					215					220			Tyr
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu
	225				230					235				Lys
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala
				245					250					255
Ser	Asn	Ser	Ala	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly
		260					265					270		Lys
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln
	275					280						285		Gln
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu
	290				295						300			Leu
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp
	305				310					315				Ala
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro
			325					330					335	Ala
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val
		340					345					350		Pro
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn
	355					360					365			Asp
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr
	370				375					380				Ala
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
	385				390					395				Arg
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			405					410					415	Val
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
	420						425					430		Ser
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	435						440					445		Phe
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
	450				455					460				Gln
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
	465				470					475				Val
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
			485					490					495	Ala
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
		500					505					510		Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	515					520						525		Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
	530					535					540			Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
	545				550				555					Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
			565					570					575	Glu
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
		580					585					590		Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
	595					600						605		Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Cys	Ile	Phe	Glu	Gln			
	610				615					620				

&lt;210&gt; 500

-583-

<211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 29 260 GCG GCG

<400> 500  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 501  
 <211> 536

-584-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 29 260 GCG GCG

&lt;400&gt; 501

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Ala Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65     70     75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85     90     95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100    105    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115    120    125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130    135    140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145    150    155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165    170    175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180    185    190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195    200    205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210    215    220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225    230    235
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245    250    255
Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260    265    270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275    280    285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290    295    300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305    310    315
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325    330    335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340    345    350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355    360    365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370    375    380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385    390    395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405    410    415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420    425    430

```

-585-

```

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 502

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 29 260 GCG GCG

&lt;400&gt; 502

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Ala Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp

```



-586-

290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 503  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 4 484 GCT GCC

<400> 503  
 Thr Ala Gly Ala Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380

-587-

```

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                               390           395           400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                               405           410           415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                               420           425           430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                               435           440           445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
                               450           455           460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                               470           475           480
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                               485           490           495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
                               500           505           510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
                               515           520           525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530                               535           540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545                               550           555           560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                               565           570           575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
                               580           585           590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595                               600           605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610                               615           620

```

&lt;210&gt; 504

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant-rep protein: rep52 4 484 GCT GCC

&lt;400&gt; 504

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1           5           10           15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20           25           30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35           40           45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50           55           60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65           70           75           80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85           90           95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

```

-588-

```

      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      305      310      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      385      390      395

```

&lt;210&gt; 505

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 4 484 GCT GCC

&lt;400&gt; 505

```

Thr Ala Gly Ala Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175

```

-589-

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 506

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 4 484 GCT GCC

&lt;400&gt; 506

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys

-590-

```

      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Ala Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 507

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 258 124 132 GCC GCC GCC

&lt;400&gt; 507

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ala Glu Pro Thr Leu
      115      120      125

```

-591-

Pro	Asn	Trp	Ala	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180				185						190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195				200						205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260				265						270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	275					280						285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			325						330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340				345						350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			405						410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	435						440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
	515					520						525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565						570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
	595						600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			

610					615					620					
<210> 508															
<211> 397															
<212> PRT															
<213> Artificial Sequence															
<220>															
<223> Mutant rep protein: rep52 258 124 132 GCC GCC GCC															
<400> 508															
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
		35					40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50				55					60					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85						90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
		115					120					125			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
	130					135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
					150					155					160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
				165					170					175	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
		195					200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
	210					215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
					230					235					240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
				245					250					255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
		275					280					285			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		290				295					300				
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
					310					315					320

-593-

<210> 509  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 258 124 132 GCC GCC GCC

<400> 509  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ala Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415



-594-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

```

<210> 510
<211> 312
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep protein: rep40 258 124 132 GCC GCC GCC

```

```

<400> 510
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val

```

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
275 280 285  
290 295  
Arg Leu Ala Arg Gly His Ser Leu  
305 310

```
<210> 511
<211> 621
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Mutant rep protein: rep78 231 497 GCC GCC
```

400> 511	Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1	Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20						25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40						45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu	
	50					55					60					
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val	
65					70					75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu	
				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
			100					105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165				170						175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	

-596-

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 512

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 231 497 GCC GCC

&lt;400&gt; 512

Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

-597-

145					150					155				160
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val
				165					170					175
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro
			180					185						190
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn
			195				200					205		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys
	210					215					220			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
225					230					235				240
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu
				245				250						255
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
		260						265					270	Ala
Ala	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
		275					280					285		Val
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
	290					295					300			Asp
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met
305					310					315				Leu
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile
				325					330					Cys
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser
			340					345					350	Glu
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys
		355					360					365		Tyr
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys
	370					375					380			Asp
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln		
385					390					395				

&lt;210&gt; 513

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 231 497 GCC GCC

&lt;400&gt; 513

Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70				75					80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
			85					90						95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160

-598-

```

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
      225      230
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250
Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys
      260      265
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      305      310
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      385      390
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490
Ala Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

&lt;210&gt; 514

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 231 497 GCC GCC

&lt;400&gt; 514

```

Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala

```

[illegible]

```
<210> 515
<211> 621
<212> PRT
<213> Artificial Sequence
```

<220>  
<223> Mutant rep protein: rep78 221 258 GCA GCC

<400>	515														
Thr	Ala	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5					10					15	
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Asn	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Thr	Glu	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75				80	
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Met	His	Val	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		

-600-

Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ala	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Ala	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
				485					490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
545					550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
				565					570					575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp

-601-

595                      600                      605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610                      615                      620

<210> 516  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 221 258 GCA GCC

<400> 516  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1                      5                      10                      15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20                      25                      30  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35                      40                      45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50                      55                      60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65                      70                      75  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85                      90                      95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100                      105                      110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115                      120                      125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130                      135                      140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145                      150                      155  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165                      170                      175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180                      185                      190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195                      200                      205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210                      215                      220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225                      230                      235  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245                      250                      255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260                      265                      270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275                      280                      285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290                      295                      300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305                      310                      315  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325                      330                      335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340                      345                      350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355                      360                      365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370                      375                      380



-602-

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 517

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 221 258 GCA GCC

&lt;400&gt; 517

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ala Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

-603-

```

385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515
Arg Leu Ala Arg Gly His Ser Leu
530          535

```

&lt;210&gt; 518

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 221 258 GCA GCC

&lt;400&gt; 518

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245          250          255

```

-604-

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

&lt;210&gt; 519

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 234 264 326 GCG GCG GCC

&lt;400&gt; 519

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro

-605-

```

      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
610      615      620

```

&lt;210&gt; 520

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 234 264 326 GCG GCG GCC

&lt;400&gt; 520

```

Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20      25      30
Ser Asn Ser Arg Ser Gln Ile Ala Ala Leu Asp Asn Ala Gly Lys
35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125

```

-606-

```

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 521

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 234 264 326 GCG GCG GCC

&lt;400&gt; 521

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

```

130						135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150					155					160	
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165					170					175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
		210				215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Ala	Gly	Ile	Thr	Ser	Glu	Lys	
225					230					235					240	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245					250					255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Ala	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
		290				295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310					315					320	
Thr	Lys	Lys	Phe	Gly	Ala	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325					330					335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala	
		370				375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	
385					390					395					400	
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405					410					415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420					425					430			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe	
		435					440					445				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln	
		450				455					460					

```
<220>
<223> Mutant rep protein: rep40 234 264 326 GCG GCG GCC
<400> 522
```

-608-

```

Met Glu Leu Val Gly Trp Leu Val Asp Ala Gly Ile Thr Ser Glu Lys
 1      5      10
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Ala Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Ala Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 523

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 153 398 AGC GCG

&lt;400&gt; 523

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu

```

				85					90					95		
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile	
		100						105					110			
Arg	Glu	Lys	Leu	Ile	Gln	Arg	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu	
		115					120					125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly	
	130					135					140					
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ser	Pro	Asn	Tyr	Leu	Leu	Pro	Lys	
145					150				155					160		
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu	
				165				170						175		
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His	
			180					185					190			
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn	
		195					200					205				
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr	
	210					215					220					
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	
225					230				235					240		
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	
				245				250						255		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys	
			260					265					270			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln	
		275					280					285				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu	
	290					295					300					
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	
305					310				315					320		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	
				325				330						335		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	
			340					345					350			
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	
		355					360					365				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu		Lys	Met	Thr	Ala	
	370					375					380					
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Ala	Val	Arg	
385					390				395					400		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val	
				405				410						415		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser	
			420													



-610-

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 524

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 153 398 AGC GCG

&lt;400&gt; 524

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr

-611-

355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 525  
 <211> 536  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep68 153 398 AGC GCG

<400> 525  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ser Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365

-612-

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 526

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 153 398 AGC GCG

&lt;400&gt; 526

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Ala Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

-613-

```

225          230          235          240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245          250          255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260          265          270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275          280          285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290          295          300
Arg Leu Ala Arg Gly His Ser Leu
305          310

```

&lt;210&gt; 527

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 53 216 GCG GCC

&lt;400&gt; 527

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20          25          30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35          40          45
Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50          55          60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65          70          75          80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85          90          95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100          105          110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115          120          125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130          135          140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145          150          155          160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165          170          175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180          185          190          195
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
200          205
Pro Asn Ser Asp Ala Pro Val Ala Arg Ser Lys Thr Ser Ala Arg Tyr
210          215          220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245          250          255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260          265          270          275
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
280          285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290          295          300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305          310          315          320

```

-614-

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 528

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 53 216 GCG GCC

&lt;400&gt; 528

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile

-615-

Arg	Glu	Lys	100	Leu	Ile	Gln	Arg	Ile	105	Tyr	Arg	Gly	Ile	Glu	110	Pro	Thr	Leu
		115						120						125				
Pro	Asn	Trp	Phe	Ala	Val	Thr	135	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly		
		130										140						
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys			
145					150					155					160			
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu			
			165						170					175				
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His			
			180					185						190				
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn			
		195					200						205					
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ala	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr			
		210				215					220							
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
225					230					235					240			
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			245						250					255				
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
			260					265					270					
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
		275					280						285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
		290				295					300							
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
305					310					315					320			
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			325						330					335				
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
			340					345					350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
		355					360					365						
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
		370				375					380							
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
385					390					395					400			
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val			
			405						410					415				
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
			420					425					430					
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
		435					440					445						
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
		450				455					460							
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
465					470					475					480			
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
			485					490						495				
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
			500					505					510					
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
		530				535												

&lt;210&gt; 529

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

-616-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 22 382 GCT GCG

&lt;400&gt; 529

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ala Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
 85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln

```

-617-

```

      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545      550      555      560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610      615      620

```

&lt;210&gt; 530

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 22 382 GCT GCG

&lt;400&gt; 530

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240

```



Glu	Val	Lys	Asp	Phe 245	Phe	Arg	Trp	Ala	Lys 250	Asp	His	Val	Val	Glu 255	Val
Glu	His	Glu	Phe 260	Tyr	Val	Lys	Lys	Gly 265	Gly	Ala	Lys	Lys	Arg 270	Pro	Ala
Pro	Ser	Asp 275	Ala	Asp	Ile	Ser	Glu 280	Pro	Lys	Arg	Val	Arg 285	Glu	Ser	Val
Ala	Gln 290	Pro	Ser	Thr	Ser	Asp 295	Ala	Glu	Ala	Ser	Ile 300	Asn	Tyr	Ala	Asp
Arg 305	Tyr	Gln	Asn	Lys 310	Cys	Ser	Arg	His	Val	Gly 315	Met	Asn	Leu	Met	Leu 320
Phe	Pro	Cys	Arg	Gln 325	Cys	Glu	Arg	Met	Asn 330	Gln	Asn	Ser	Asn	Ile 335	Cys
Phe	Thr	His	Gly 340	Gln	Lys	Asp	Cys	Leu 345	Glu	Cys	Phe	Pro	Val 350	Ser	Glu
Ser	Gln	Pro 355	Val	Ser	Val	Val	Lys 360	Lys	Ala	Tyr	Gln	Lys 365	Leu	Cys	Tyr
Ile 370	His	His	Ile	Met	Gly	Lys 375	Val	Pro	Asp	Ala	Cys 380	Thr	Ala	Cys	Asp
Leu 385	Val	Asn	Val	Asp	Leu 390	Asp	Asp	Cys	Ile	Phe 395	Glu	Gln			

<220>  
<223> Mutant rep protein: rep68 22 382 GCT GCG

<400>	531																
Thr	Ala	Gly	Phe	Tyr <sub>5</sub>	Glu	Ile	Val	Ile	Lys <sub>10</sub>	Val	Pro	Ser	Asp	Leu <sub>15</sub>	Asp		
1																	
Glu	His	Leu	Pro	Gly <sub>20</sub>	Ala	Ser	Asp	Ser <sub>25</sub>	Phe	Val	Asn	Trp	Val <sub>30</sub>	Ala	Glu		
Lys	Glu	Trp <sub>35</sub>	Glu	Leu	Pro	Pro	Asp <sub>40</sub>	Ser	Asp	Met	Asp	Leu <sub>45</sub>	Asn	Leu	Ile		
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala <sub>55</sub>	Glu	Lys	Leu	Gln <sub>60</sub>	Arg	Asp	Phe	Leu		
Thr	Glu	Trp	Arg	Arg	Val <sub>70</sub>	Ser	Lys	Ala	Pro	Glu <sub>75</sub>	Ala	Leu	Phe	Phe	Val <sub>80</sub>		
65																	
Gln	Phe	Glu	Lys	Gly <sub>85</sub>	Glu	Ser	Tyr	Phe	His <sub>90</sub>	Met	His	Val	Leu	Val <sub>95</sub>	Glu		
Thr	Thr	Gly	Val <sub>100</sub>	Lys	Ser	Met	Val	Leu <sub>105</sub>	Gly	Arg	Phe	Leu	Ser <sub>110</sub>	Gln	Ile		
Arg	Glu	Lys <sub>115</sub>	Leu	Ile	Gln	Arg	Ile <sub>120</sub>	Tyr	Arg	Gly	Ile	Glu <sub>125</sub>	Pro	Thr	Leu		
Pro	Asn	Trp	Phe	Ala	Val	Thr <sub>135</sub>	Lys	Thr	Arg	Asn <sub>140</sub>	Gly	Ala	Gly	Gly	Gly		
Asn	Lys	Val	Val	Asp	Glu <sub>150</sub>	Cys	Tyr	Ile	Pro	Asn <sub>155</sub>	Tyr	Leu	Leu	Pro	Lys <sub>160</sub>		
145																	
Thr	Gln	Pro	Glu	Leu <sub>165</sub>	Gln	Trp	Ala	Trp <sub>170</sub>	Thr	Asn	Met	Glu	Gln	Tyr <sub>175</sub>	Leu		
Ser	Ala	Cys	Leu <sub>180</sub>	Asn	Leu	Thr	Glu	Arg <sub>185</sub>	Lys	Arg	Leu	Val	Ala <sub>190</sub>	Gln	His		
Leu	Thr	His <sub>195</sub>	Val	Ser	Gln	Thr	Gln <sub>200</sub>	Glu	Gln	Asn	Lys	Glu <sub>205</sub>	Asn	Gln	Asn		
Pro	Asn	Ser	Asp	Ala	Pro	Val <sub>215</sub>	Ile	Arg	Ser	Lys	Thr <sub>220</sub>	Ser	Ala	Arg	Tyr		
Met	Glu	Leu	Val	Gly <sub>230</sub>	Trp	Leu	Val	Asp	Lys	Gly <sub>235</sub>	Ile	Thr	Ser	Glu	Lys <sub>240</sub>		
225																	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala		

[illegible]

<220>  
<223> Mutant rep protein: rep40 22 382 GCT GCG

<400> 532															
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
	35						40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
	50					55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70					75				80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
				85					90					95	
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100					105					110		

-620-

```

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Ala Thr Ala
      145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      290      295      300
Arg Leu Ala Arg Gly His Ser Leu
      305      310

```

&lt;210&gt; 533

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 231 411 GCC GCA

&lt;400&gt; 533

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
      145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn

```

-621-

Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
210						215					220				
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340				345						350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ala	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420				425						430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485					490						495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Tyr	Gln	Asn	Lys	Cys	Ser	Arg	His	Val	Gly	Met	Asn	Leu	Met	Leu
	530					535					540				
Phe	Pro	Cys	Arg	Gln	Cys	Glu	Arg	Met	Asn	Gln	Asn	Ser	Asn	Ile	Cys
	545				550					555					560
Phe	Thr	His	Gly	Gln	Lys	Asp	Cys	Leu	Glu	Cys	Phe	Pro	Val	Ser	Glu
			565					570						575	
Ser	Gln	Pro	Val	Ser	Val	Val	Lys	Lys	Ala	Tyr	Gln	Lys	Leu	Cys	Tyr
			580					585					590		
Ile	His	His	Ile	Met	Gly	Lys	Val	Pro	Asp	Ala	Cys	Thr	Ala	Cys	Asp
		595					600					605			
Leu	Val	Asn	Val	Asp	Leu	Asp	Asp	Cys	Ile	Phe	Glu	Gln			
	610					615					620				

&lt;210&gt; 534

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 231 411 GCC GCA

-622-

<400> 534  
 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 535

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 231 411 GCC GCA

&lt;400&gt; 535

-623-

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ala Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala

-624-

Pro	Ser	Asp	Ala	485	Asp	Ile	Ser	Glu	Pro	490	Lys	Arg	Val	Arg	Glu	495	Ser	Val
			500						505						510			
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
		515					520					525						
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	530					535												

&lt;210&gt; 536

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 231 411 GCC GCA

&lt;400&gt; 536

Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys			
1				5				10						15				
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala			
			20					25					30					
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys			
		35					40					45						
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln			
	50					55					60							
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu			
	65					70				75				80				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala			
			85					90					95					
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala			
			100					105					110					
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro			
		115					120					125						
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp			
	130					135					140							
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala			
	145				150				155					160				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg			
			165					170						175				
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ala	Asp	Pro	Thr	Pro	Val			
		180						185					190					
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser			
	195						200					205						
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe			
	210				215						220							
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln			
	225				230					235					240			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val			
			245					250						255				
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala			
		260						265					270					
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val			
	275						280					285						
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp			
	290					295					300							
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu											
	305				310													

&lt;210&gt; 537

&lt;211&gt; 621

&lt;212&gt; PRT

-625-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 59 305 GCG GCC

&lt;400&gt; 537

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Ala Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

```



-626-

```

      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
  500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
  530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
  545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
  580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
  595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
  610      615      620

```

&lt;210&gt; 538

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 59 305 GCG GCC

&lt;400&gt; 538

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
      85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220

```

-627-

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 539

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 59 305 GCG GCC

&lt;400&gt; 539

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Ala Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys

-628-

```

225          230          235          240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
                260
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
                275
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
                290
Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305          310          315          320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
                340
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
                355
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370          375          380          385
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
                420
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
                435
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450          455          460          465
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500          505          510          515
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515          520          525          530
Arg Leu Ala Arg Gly His Ser Leu
                535

```

&lt;210&gt; 540

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 59 305 GCG GCC

&lt;400&gt; 540

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20          25          30          35
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35          40          45          50
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50          55          60          65
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65          70          75          80
Ala Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85          90          95

```

-629-

```

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      100      105
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      115      120
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
      165      170
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Leu Ala Arg Gly His Ser Leu
305      310

```

&lt;210&gt; 541

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 53 231 GCG GCC

&lt;400&gt; 541

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

```

Leu	Thr	His	180														
		195	Val	Ser	Gln	Thr	Gln	185									190
Pro	Asn		200	Ala	Pro	Val	Ile	Glu	Gln	Asn	Lys	Glu	205	Asn	Gln	Asn	
	210	Ser	Asp			215		Arg	Ser	Lys	Thr	Thr	Ser	Ala	Arg	Tyr	
Met	Glu	Leu	Val	Gly	Trp	Ala	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys	240	
225			245		230					235							
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala	255	
			260	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys		
Ser	Asn	Ser	Arg					265						270			
		275	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln		
Ile	Met	Ser					280					285					
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu		
	290					295					300						
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala	320	
305					310					315							
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala	335	
			325						330								
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro		
			340					345				350					
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp		
		355					360					365					
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala		
	370					375					380						
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	400	
385					390					395							
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val		
			405					410						415			
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser		
			420					425					430				
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe		
		435					440					445					
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln		
	450					455					460						
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val	480	
465				470						475							
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala		
			485					490						495			
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val		
			500					505					510				
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp		
		515															

```
<210> 542
<211> 397
<212> PRT
<213> Artificial Sequence
```

-631-

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 53 231 GCG GCC

&lt;400&gt; 542

```

Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315      320
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 543

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-632-

&lt;223&gt; Mutant rep protein: rep68 53 231 GCG GCC

&lt;400&gt; 543

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Ala Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
 85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450      455      460

```

-633-

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

<210> 544  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 53 231 GCG GCC

<400> 544  
 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310



-634-

<210> 545  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 258 498 GCC GCT

<400> 545  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415

-635-

```

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
      610      615      620

```

<210> 546  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep proteinrep 52 258 498 GCC GCT

```

<400> 546
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  20      25      30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

-636-

```

      195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225      230      235
Glu Val Lys Asp Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      260      265      270
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290      295      300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305      310      315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      325      330      335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      340      345      350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      355      360      365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370      375      380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385      390      395

```

&lt;210&gt; 547

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 258 498 GCC GCT

&lt;400&gt; 547

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205

```

-637-

```

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
  210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
 385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
 465      470      475      480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
 530      535

```

&lt;210&gt; 548

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 258 498 GCC GCT

&lt;400&gt; 548

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      20      25      30
Ser Ala Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu

```

-638-

```

65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100         105         110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115         120         125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130         135         140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145         150         155         160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165         170         175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180         185         190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195         200         205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210         215         220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225         230         235         240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245         250         255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260         265         270
Pro Ala Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275         280         285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290         295         300
Arg Leu Ala Arg Gly His Ser Leu
305         310

```

&lt;210&gt; 549

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 88 231 GCC GCC

&lt;400&gt; 549

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1          5          10          15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20         25         30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35         40         45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50         55         60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65         70         75         80
Gln Phe Glu Lys Gly Glu Ser Ala Phe His Met His Val Leu Val Glu
85         90         95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100        105        110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115        120        125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130        135        140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145        150        155        160

```

-639-

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375 380  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390 395 400  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410 415  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425 430  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440 445  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455 460  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470 475 480  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490 495  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505 510  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520 525  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 530 535 540  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 545 550 555 560  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 565 570 575  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 580 585 590  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 595 600 605  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 610 615 620

&lt;210&gt; 550

&lt;211&gt; 397

-640-

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 88 231 GCC GCC

&lt;400&gt; 550

```

Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
 1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35      40      45
Ile Met Ser Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65      70      75
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225     230     235
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290     295     300
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305     310     315
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
325     330     335
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
340     345     350
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
355     360     365
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
370     375     380
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385     390     395

```

&lt;210&gt; 551

&lt;211&gt; 536

&lt;212&gt; PRT

-641-

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 88 231 GCC GCC

&lt;400&gt; 551

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Ala Phe His Met His Val Leu Val Glu
85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe

```



-642-

```

      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Leu Ala Arg Gly His Ser Leu
      530      535

```

<210> 552  
 <211> 312  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep40 88 231 GCC GCC

```

<400> 552
Met Glu Leu Val Gly Trp Ala Val Asp Lys Gly Ile Thr Ser Glu Lys
  1      5      10      15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
  20      25      30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
  35      40      45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
  50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
  65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
  85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
  100      105      110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
  115      120      125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
  130      135      140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
  145      150      155      160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
  165      170      175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
  180      185      190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
  195      200      205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
  210      215      220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
  225      230      235      240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
  245      250      255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
  260      265      270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
  275      280      285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
  290      295      300

```

-643-

Arg Leu Ala Arg Gly His Ser Leu  
305 310

&lt;210&gt; 553

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 101 363 GCA GCC

&lt;400&gt; 553

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
 145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
      165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
      180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
      195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
      210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
      245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
      260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
      275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
      290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
      325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
      340      345      350
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
      355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
 370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg

```

-644-

```

385          390          395          400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
         405          410          415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
         420          425          430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
         435          440          445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
         450          455          460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
         465          470          475          480
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
         485          490          495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
         500          505          510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
         515          520          525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
         530          535          540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
         545          550          555          560
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
         565          570          575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
         580          585          590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
         595          600          605
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
         610          615          620

```

&lt;210&gt; 554

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep52 101 363 GCA GCC

&lt;400&gt; 554

```

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
 1          5          10          15
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
 20          25          30
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
 35          40          45
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
 50          55          60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
 65          70          75          80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
 85          90          95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100          105          110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115          120          125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
130          135          140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145          150          155          160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165          170          175

```

-645-

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

&lt;210&gt; 555

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 101 363 GCA GCC

&lt;400&gt; 555

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Ala Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His

-646-

Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		180						185					190		
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
	210					215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225					230					235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
	290					295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305					310					315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Tyr	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Ala	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
	370					375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385					390					395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
	450					455					460				
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465					470					475					480
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			485						490					495	
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			500					505					510		
Ala	Gln	Pro	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala	Asp
		515					520					525			
Arg	Leu	Ala	Arg	Gly	His	Ser	Leu								
	530					535									

&lt;210&gt; 556

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 101 363 GCA GCC

&lt;400&gt; 556

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25				30			
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			35				40					45			

-647-

```

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50      55      60
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65      70      75      80
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85      90      95
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100     105     110
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115     120     125
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Ala Phe Pro Phe Asn Asp
130     135     140
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145     150     155     160
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165     170     175
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180     185     190
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195     200     205
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210     215     220
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225     230     235     240
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245     250     255
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260     265     270
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275     280     285
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290     295     300
Arg Leu Ala Arg Gly His Ser Leu
305     310

```

&lt;210&gt; 557

&lt;211&gt; 621

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep78 354 132 GCC GCC

&lt;400&gt; 557

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
20     25     30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35     40     45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50     55     60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65     70     75     80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85     90     95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100    105    110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115    120    125
Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly

```

	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Gln	Tyr	Leu
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Thr	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		
Leu	Thr	His	Val	Ser	Gln	Thr	Gln	Glu	Gln	Asn	Lys	Glu	Asn	Gln	Asn
		195					200					205			
Pro	Asn	Ser	Asp	Ala	Pro	Val	Ile	Arg	Ser	Lys	Thr	Ser	Ala	Arg	Tyr
		210				215					220				
Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
225				230						235					240
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
				245					250					255	
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			260					265					270		
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
		275					280					285			
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
		290				295					300				
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
305				310						315					320
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
				325					330					335	
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			340					345					350		
Phe	Ala	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
		355					360					365			
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
		370				375					380				
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
385				390						395					400
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
				405					410					415	
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			420					425					430		
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435					440					445			
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
		450				455						460			
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
465				470						475				480	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala

-649-

<210> 558  
 <211> 397  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep52 354 132 GCC GCC

<400> 558  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 1 5 10 15  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 20 25 30  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 35 40 45  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 50 55 60  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 65 70 75 80  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 85 90 95  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 100 105 110  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 115 120 125  
 Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 130 135 140  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 145 150 155 160  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 165 170 175  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 180 185 190  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 195 200 205  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 210 215 220  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 225 230 235 240  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 245 250 255  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 260 265 270  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 275 280 285  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu  
 305 310 315 320  
 Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys  
 325 330 335  
 Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu  
 340 345 350  
 Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr  
 355 360 365  
 Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp  
 370 375 380  
 Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln  
 385 390 395

<210> 559



-650-

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 354 132 GCC GCC

&lt;400&gt; 559

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
 20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
 35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
 50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
 65      70      75      80
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
 85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115      120      125
Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165      170      175
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180      185      190
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195      200      205
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210      215      220
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225      230      235      240
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245      250      255
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260      265      270
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275      280      285
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290      295      300
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305      310      315      320
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325      330      335
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340      345      350
Phe Ala Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355      360      365
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395      400
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser

```

-651-

Thr	Thr	Phe	420	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
		435	Glu	Arg	Leu	Asp	440	His	Asp	Phe	Gly	Lys	Val	Thr	Lys
Glu	Leu	Thr	450	Arg	Phe	Arg	455	Trp	Ala	Lys	Asp	460	His	Val	Val
Glu	Val	Lys	465	Asp	470	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
Glu	His	Glu	485	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro
Pro	Ser	Asp	500	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser
Ala	Gln	Pro	515	Ser	Thr	Ser	Asp	Ala	Glu	Ala	Ser	Ile	Asn	Tyr	Ala
Arg	Leu	Ala	530	Arg	Gly	His	Ser	Leu							

&lt;210&gt; 560

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep40 354 132 GCC GCC

&lt;400&gt; 560

Met	Glu	Leu	Val	Gly	Trp	Leu	Val	Asp	Lys	Gly	Ile	Thr	Ser	Glu	Lys
1				5					10					15	
Gln	Trp	Ile	Gln	Glu	Asp	Gln	Ala	Ser	Tyr	Ile	Ser	Phe	Asn	Ala	Ala
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Gly	Lys
			35				40					45			
Ile	Met	Ser	Leu	Thr	Lys	Thr	Ala	Pro	Asp	Tyr	Leu	Val	Gly	Gln	Gln
			50			55					60				
Pro	Val	Glu	Asp	Ile	Ser	Ser	Asn	Arg	Ile	Tyr	Lys	Ile	Leu	Glu	Leu
65					70				75					80	
Asn	Gly	Tyr	Asp	Pro	Gln	Tyr	Ala	Ala	Ser	Val	Phe	Leu	Gly	Trp	Ala
			85					90					95		
Thr	Lys	Lys	Phe	Gly	Lys	Arg	Asn	Thr	Ile	Trp	Leu	Phe	Gly	Pro	Ala
			100				105						110		
Thr	Thr	Gly	Lys	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro
			115				120					125			
Phe	Ala	Gly	Cys	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp
			130			135					140				
Cys	Val	Asp	Lys	Met	Val	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Ala
145					150				155					160	
Lys	Val	Val	Glu	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg
			165					170					175		
Val	Asp	Gln	Lys	Cys	Lys	Ser	Ser	Ala	Gln	Ile	Asp	Pro	Thr	Pro	Val
			180					185					190		
Ile	Val	Thr	Ser	Asn	Thr	Asn	Met	Cys	Ala	Val	Ile	Asp	Gly	Asn	Ser
			195				200					205			
Thr	Thr	Phe	Glu	His	Gln	Gln	Pro	Leu	Gln	Asp	Arg	Met	Phe	Lys	Phe
			210			215					220				
Glu	Leu	Thr	Arg	Arg	Leu	Asp	His	Asp	Phe	Gly	Lys	Val	Thr	Lys	Gln
225					230				235					240	
Glu	Val	Lys	Asp	Phe	Phe	Arg	Trp	Ala	Lys	Asp	His	Val	Val	Glu	Val
			245					250						255	
Glu	His	Glu	Phe	Tyr	Val	Lys	Lys	Gly	Gly	Ala	Lys	Lys	Arg	Pro	Ala
			260					265					270		
Pro	Ser	Asp	Ala	Asp	Ile	Ser	Glu	Pro	Lys	Arg	Val	Arg	Glu	Ser	Val
			275				280					285			

-652-

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 290 295 300  
 Arg Leu Ala Arg Gly His Ser Leu  
 305 310

<210> 561  
 <211> 621  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep protein: rep78 10 132 GCG GCC

<400> 561  
 Thr Ala Gly Phe Tyr Glu Ile Val Ile Ala Val Pro Ser Asp Leu Asp  
 1 5 10 15  
 Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu  
 20 25 30  
 Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile  
 35 40 45  
 Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu  
 50 55 60  
 Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val  
 65 70 75 80  
 Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu  
 85 90 95  
 Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile  
 100 105 110  
 Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu  
 115 120 125  
 Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly  
 130 135 140  
 Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys  
 145 150 155 160  
 Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170 175  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185 190  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200 205  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215 220  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230 235 240  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250 255  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265 270  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280 285  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295 300  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310 315 320  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330 335  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345 350  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360 365  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

-653-

```

      370      375      380
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385      390      395
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
      405      410      415
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
      420      425      430
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
      435      440      445
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
      450      455      460
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
      465      470      475
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
      485      490      495
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
      500      505      510
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
      515      520      525
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
      530      535      540
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
      545      550      555
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
      565      570      575
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
      580      585      590
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
      595      600      605
Leu Val Asn Val Asp Leu Asp Cys Ile Phe Glu Gln
      610      615      620

```

&lt;210&gt; 562

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep protein: rep68 10 132 GCG GCC

&lt;400&gt; 562

```

Thr Ala Gly Phe Tyr Glu Ile Val Ile Ala Val Pro Ser Asp Leu Asp
1      5      10      15
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
      20      25      30
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
      35      40      45
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
      50      55      60
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
      65      70      75
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
      85      90      95
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
      100      105      110
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
      115      120      125
Pro Asn Trp Ala Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
      130      135      140
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145      150      155      160

```

-654-

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu  
 165 170  
 Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His  
 180 185  
 Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn  
 195 200  
 Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr  
 210 215  
 Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys  
 225 230  
 Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala  
 245 250  
 Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys  
 260 265  
 Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln  
 275 280  
 Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu  
 290 295  
 Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala  
 305 310  
 Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala  
 325 330  
 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro  
 340 345  
 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp  
 355 360  
 Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala  
 370 375  
 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg  
 385 390  
 Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val  
 405 410  
 Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser  
 420 425  
 Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe  
 435 440  
 Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln  
 450 455  
 Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val  
 465 470  
 Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala  
 485 490  
 Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val  
 500 505  
 Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp  
 515 520  
 Arg Leu Ala Arg Gly His Ser Leu  
 530 535

&lt;210&gt; 563

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 4 GCT

&lt;400&gt; 563

acggcggggg cttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc  
 ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat  
 tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag

60

120

180

-655-

cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaactc	acccgcgcgt	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtagggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcattg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	atcatatcat	gggaaagggtg	gggaaagggtg	1800
ccagacgctt	cgactgcctg	cgatctggtc	aatgtggatt	tggtgatctg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 564

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant\_rep DNA sequence: 10 GCG

&lt;400&gt; 564

acggcggggt	tttacgagat	tgtgattgag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggaatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260

-656-

aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 565

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 20 GCC

&lt;400&gt; 565

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctggcc	60
ggcattttctg	acagcttttg	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtgc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcgccttc	caactcgctg	780
tcccaaatca	aggctgcctt	ggacaatgct	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccca	tatgcgcgtt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggtg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 566

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-657-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 22 GCT

&lt;400&gt; 566

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcgcttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggttg ctctgtggca aggggattac ctcggaagag 720
cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taaacgggtg cgaatcccaa tatgcggctt ccgtctttct gggatggggc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctccggccag atagaccoga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gaccgcgcc cagtgcgca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaaga ctgttttagag tgctattccc tgcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgtg tcagaaactg tgctacattc atcatatcat gggaaaggtg 1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 567

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 29 GCG

&lt;400&gt; 567

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcatttctg acagctttgt gaacgcgggt gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggttg ctctgtggca aggggattac ctcggaagag 720
cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840

```



-658-

cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcccgtt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaactc	acccgcctgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtagggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgthttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaaggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 568

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 38 GCG

&lt;400&gt; 568

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	ggcgccagat	120
tctgacatgg	atctgaatct	gatttgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tcgggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgacagtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatcacgt	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgc	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcccgtt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaactc	acccgcctgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtagggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgthttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaaggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920

-659-

cactctctct ga

1932

&lt;210&gt; 569

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 39 GCA

&lt;400&gt; 569

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccggcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttgga	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccgaag	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaaacaa	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgtacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	ctccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 570

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 53 GCT

&lt;400&gt; 570

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccggcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccgcta	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420

-660-

gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccaa	tatgcggcctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcctgc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tgatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 571

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 59 GCG

&lt;400&gt; 571

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaaggcgag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccaa	tatgcggcctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcctgc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500

-661-

gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttccctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 572

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 64 GCT

&lt;400&gt; 572

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttg	ctacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaaccaagg	ggtggatgag	tgctacatcc	ccaattactt	gtccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcgagaag	720
cagtggatcc	aggaggacca	ggcctcatal	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	cgaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttccctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 573

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 74 GCG

&lt;400&gt; 573

-662-

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccg	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtgggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aaactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgcgt	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtagggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gataataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 574

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 86 GCG

&lt;400&gt; 574

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagcgag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080

-663-

aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gataataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 575

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 88 GCC

&lt;400&gt; 575

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	cgcttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accacgctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccaact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gataataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 576

&lt;211&gt; 1932

-664-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 101 GCA

&lt;400&gt; 576

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
gcatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacc	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgctg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaaaccgggt	cgatcccca	tatgcggctt	ccgtctttct	gggatgggct	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctt	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccc	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaaact	acccgcgctc	tgatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggttgga	gccaaagaaa	gacccgcccc	cagtgaacga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthtccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgctcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tgatgatctg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 577

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 124 GCC

&lt;400&gt; 577

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcgggg	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacc	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660

-665-

tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtgatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaactc	acccgcctgc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aactctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgtg	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 578

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 125 GCG

&lt;400&gt; 578

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactcgcgc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgcgcgcgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cgggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtgatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tggtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaactc	acccgcctgc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aactctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740



-666-

tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaaggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 579  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 127 GCT

<400> 579						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtgggc	cagcatctga	cgacgtgtgc	gcagacgcag	600
gagcagaaca	aaggaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaacc	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aaactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggttgga	gccaaagaaa	gaccgcggcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaatcc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaaggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 580  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 132 GCC

<400> 580						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240

-667-

caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagatttcgcg	aaaaactgat	tcagagaatt	360
taccgcgggg	tcgagccgac	tttgccaaac	tgggcccgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacagtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatac	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaaccgggt	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcgggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcgcc	cagtgcgcga	1500
gataataagt	agcccaaacc	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcacccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 581

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 140 GCC

&lt;400&gt; 581

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagatttcgcg	aaaaactgat	tcagagaatt	360
taccgcgggg	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatgcc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacagtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatac	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaaccgggt	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcgggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320

-668-

ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgaacga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 582

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 161 GCC

&lt;400&gt; 582

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
gcccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcgagagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaaac	taaacgggta	cgatccccc	tatgcccgtt	ccgtctttct	gggatgggoc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgaacga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 583

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-669-

&lt;223&gt; Mutant rep DNA sequence: 163 GCT

```

<400> 583
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttcac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccaggctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccagggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc agggagacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840
cccgactacc tggtagggcca gcagccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtggaaac taaacgggta cgatcccaa tatcggtt ccgtctttct ggatggggc 960
acgaaaaaag tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgccttct acgggtgctg aaactggacc 1080
aatgagaact ttccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaagggtcgt ggagtgcggc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccgag atagaccgga ctcccgatg ctcaactcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atthtgaact acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agacttttc cggtagggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcccc cagtgcgca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagtgcgc agccatcgac gtgagacgcg 1560
gaagcttgcg tcaactacgc agacaggtac caaaacaaat gttctcgta cgtgggcgatg 1620
aatctgatgc tgttccctg cagacaatgc tgctacatcc atcagaatcc aaatatctgc 1680
ttcactcagc gacagaaaga ctgttttagag tgcttcccg tgcagaatc tcaaccggt 1740
tctgtcgtga aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagcgcctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 584

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 175 GCT

```

<400> 584
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttcac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccaggctg agctccagtg ggcgtggact aatatggaac aggttttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccagggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc agggagacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840
cccgactacc tggtagggcca gcagccgtg gaggacattt ccagcaatcg gatttataaa 900

```

-670-

atthttggaac	taaacgggta	cgatcccaa	tatgcccgtt	ccgtttttct	gggatgggccc	960
acgaaaaagt	tccgcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtctgcg	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 585

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 193 GCG

&lt;400&gt; 585

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcgggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcgg	ggaacaaagt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtattttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatgcga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggat tac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgccg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaa	tatgcccgtt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tccgcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtctgcg	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

-671-

<210> 586  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 196 GCC

```

<400> 586
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa      480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgcctc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcgagagaag      720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg      780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900
attttggaac taaacgggta cgatcccaaa tatgcgcgtt ccgtctttct gggatgggccc      960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag      1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc      1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg      1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc      1200
gtggaccaga aatgcaagtc ctcgcccagc atagaccgca ccttcgaaca ccagcagccg      1260
aacaccaaca tgtgcgcgtg gattgacggg aactcaacga ctttcgaaca ccagcagccg      1320
ttgcaagacc ggatgttcaa atttgaatc acccgccgtc tggatcatga ctttgggaag      1380
gtcaccaagc aggaagtcaa agactttttc cgggtggcaa aggatcacgt ggttgaggtg      1440
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg      1500
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg      1560
aatctgatgc tgtttccctg cagacaatgc ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt      1620
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt      1680
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaaggtg      1740
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa      1800
caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga      1860
cactctctct ga                                     1920
                                     1932

```

<210> 587  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 197 GCC

```

<400> 587
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa      480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg      540

```

-672-

aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtggc	ccagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaactc	acccgccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 588

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 GCA

&lt;400&gt; 588

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggtg	300
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcgggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
gcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaactc	acccgccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	gggtgaggtg	1440
gatcatgaat	tctacgtcaa	aaaggggtga	gccaagaaaa	gacccgcccc	cagtgcagca	1500
gacataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620

-673-

aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 589  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 228 GCG

<400> 589						
acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgagg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	ggttggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggcgggggtg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtacc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaaagggtg	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgagg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcccgt	gattgacggg	aaactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggtgtttcaa	atttgaaact	acccgcggtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 590  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 231 GCC

<400> 590						
acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120



-674-

tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	gccgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtgggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
atthtgggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggccccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgaacga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctctgca	cgtgggcatg	1620
aatctgatgc	tgthtccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcatgcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtctgtc	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 591

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 234 GCG

&lt;400&gt; 591

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggacg	cggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtgggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
atthtgggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200

-675-

gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacy	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 592

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 237 GCC

&lt;400&gt; 592

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagt	gggtggatgag	tgctacatcc	ccaattactt	gtccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattgc	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacy	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 592

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-676-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 250 GCC

&lt;400&gt; 593

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa      480
accagcctg agctccagt ggcgtggact aatatggaac agtatttaag cgctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcgagagaag      720
cagtggatcc aggaggacca ggccctcagcc atctccttca atgcggcctc caactcgcgg      780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgactacc tgggtgggcca gcagcccctg gaggacattt ccagcaatcg gatttataaa      900
attttggaaac taaacgggta cgatcccaa tatcgcgctt cgtctttctt gggatgggcc      960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag      1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc      1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg      1140
aagatgaccg ccaaggctgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc      1200
gtggaccaga aatgcaagtc ctcgcccgag atagaccoga ctcccgtgat cgtcacctcc      1260
aacaccaaca tgtgcgcctg gattgacggg aactcaacga ccttcgaaca ccagcagccg      1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag      1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg      1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gacccgcccc cagtgcgcga      1500
gatataagtg agcccaaacg ggtgcgcgag caaaacaaat gttctcgtca cgtgggcatg      1560
gaagcttcga tcaactacgc agacaggtac gagagaatga atcagaattc aaatatctgc      1620
aatctgatgc tgtttccctg cagacaatgc gagagaaact tgctttcccg tgtcagaatc tcaaccggtt      1680
ttcactcacg gacagaaaga ctgttttagag tgcattacatt atcatatcat gggaaaggtg      1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg      1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa      1860
caataaatga tttaaatcag gtatgggtgc cgatggttat cttccagatt ggctcgagga      1920
cactctctct ga                                     1932

```

&lt;210&gt; 594

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 258 GCC

&lt;400&gt; 594

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa      480
accagcctg agctccagt ggcgtggact aatatggaac agtatttaag cgctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcgagagaag      720
cagtggatcc aggaggacca ggccctcagcc atctccttca atgcggcctc cgctcgcgg      780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840

```

-677-

cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 595

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 260 GCG

&lt;400&gt; 595

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactcgtccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	cgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttcac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gthgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcggcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920

-678-

cactctctct ga

1932

<210> 596  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 263 GCC

<400> 596  
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgctg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaagaag 720  
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcgg 780  
tcccaaggcca aggcgtcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840  
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
atthttggaac taaacgggta cgatccccaat tatgcggctt ccgtctttct gggatgggccc 960  
acgaaaaagt tcggcaagag gaacaccatc aaagccattc ggcctgcaac taccgggaag 1020  
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080  
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggagggaag caagggtcgc 1200  
gtggaccaga aatgcaagtc ctcgcccag atagaccgga ctcccgtgat cgtcacctcc 1260  
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380  
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg 1440  
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gacccgcccc cagtgcagca 1500  
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620  
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaatc aaatatctgc 1680  
ttcactcacg gacagaaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccgtt 1740  
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800  
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860  
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

<210> 597  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 264 GCG

<400> 597  
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgctg tcacaaagac cagaaatggc 420

-679-

gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatcg	cggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcctttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcctgc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtgtgcg	agccatcgac	gtcagacgcg	1560
gaagcttctga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthtccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgatcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aactgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcagga	1920
cactctctct	ga					1932

&lt;210&gt; 598

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 334 GCG

&lt;400&gt; 598

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatthtctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	cgctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcctttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcctgc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500

-680-

gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 599  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 335 GCT

<400> 599						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gtccccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgacag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	gggctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 600  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 337 GCT

<400> 600

-681-

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag      180
cgcgacttttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caattttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa      480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg      540
aatctcacgg agcgtaaacg gttgggtggc cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cgggtgatcag atcaaaaact      660
tcagccagggt acatggagct ggtcgggttg ctctgggaca aggggattac ctcggaagag      720
cagtggtatcc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg      780
tccccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900
atthttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc      960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcagc taccgggaag      1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc      1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg      1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc      1200
gtggaccaga aatgcaagtc ctcgccccag atagaccgga ctcccgtgat cgtcacctoc      1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg      1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag      1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg      1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcggcc cagtgcgca      1500
gatataagtg agcccaaacg ggtgcgcgag caaaacaaat gttctcgtca cgtgggcatg      1560
gaagcttcga tcaactacgc agacaggtac gagagaatga atcagaattc aaatatctgc      1620
aatctgatgc tgtttccctg cagacaatgc tgctttcccg tgtcagaatc tcaaccggtt      1680
ttcactcacg gacagaaaaga ctggttagag tgcttccatc atcatatcat gggaaagggtg      1740
tctgtcgtca aaaaggcgta tcagaaaactg aatgtggatt tggatgactg catctttgaa      1800
ccagacgctt gcaactgcctg cgatctggtc cgatggttat cttccagatt ggctcgagga      1860
caataaatga tttaaatcag gtatgggtgc cgtatggttat cttccagatt ggctcgagga      1920
cactctctct ga

```

&lt;210&gt; 601

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 341 GCC

&lt;400&gt; 601

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag      180
cgcgacttttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caattttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa      480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg      540
aatctcacgg agcgtaaacg gttgggtggc cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cgggtgatcag atcaaaaact      660
tcagccagggt acatggagct ggtcgggttg ctctgggaca aggggattac ctcggaagag      720
cagtggtatcc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg      780
tccccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900
atthttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc      960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcagc taccgggaag      1020
gccaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc      1080

```



-682-

```

aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctccggcccag atagaccgga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gacccgcccc cagtgcgcga 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatgggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 602

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 342 GCC

&lt;400&gt; 602

```

acggcggggt ttacagagat tgtgattaag gtccccagcg accttgacga gcactctgcc 60
ggcattttctg acagctttgt gaactcgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgcctgtgt agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatattaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcgagagaag 720
cagtggatcc aggaggacca ggctcctac atctccttca atgcggcctc caactcgccg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
attttggaac taaacgggta cgatcccca tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggtccttct acgggtgact aaactggacc 1020
accgccatcg cggaggccat agcccacact gtgcccttct gacaagatgg tgatctggtg ggaggagggg 1140
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg aaagccattc tcggaggaag caaggtgcgc 1200
aagatgaccg ccaaggtcgt ggagtcggcc atagaccgga ctcccgtgat cgtcacctcc 1260
gtggaccaga aatgcaagtc ctccggcccag atagaccgga ccttcgaaca ccagcagccg 1320
aacaccaaca tgtgcgccgt gattgacggg aactcaacga acccgccgtc tggatcatga ctttgggaag 1380
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc cggatcatga ggttgagggtg 1440
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg 1500
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gacccgcccc cagtgcgcga 1560
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1620
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1680
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1740
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1800
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1860
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1920
caataaatga tttaaatcag gtatggctgc cgatgggttat cttccagatt ggctcgagga 1932
cactctctct ga

```

&lt;210&gt; 603

&lt;211&gt; 1932

-683-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 347 GCA

&lt;400&gt; 603

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgag	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthtggaa	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccgc	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aaactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	caagtgtcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgtg	tcagaaaactg	tggtacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 604

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 AAT

&lt;400&gt; 604

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgag	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660

-684-

tcagccaggt	acatggagct	ggtcgggtgg	ctctgggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacaat	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaagggcgt	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 605

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 GCT

&lt;400&gt; 605

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttcac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctctgag	cagatttcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacgct	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccga	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740

-685-

tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcagagga	1920
cactctctct	ga					1932

<210> 606  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 354 GCC

<400> 606						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
aatgtggaac	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttcg	ccgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcagca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaatc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcagagga	1920
cactctctct	ga					1932

<210> 607  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 363 GCC

<400> 607						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240

-686-

caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tctggaagac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcgggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgaggcct	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgttg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgccgtc	tgatcatga	ctttgggaag	1380
gtcacaagc	aggaagtcga	agactttttc	cgggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcagagga	1920
cactctctct	ga					1932

&lt;210&gt; 608

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 364 GCT

&lt;400&gt; 608

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tctggaagac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcgggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaacg	ctcccttcaa	cgactgtgtc	gacaagatgg	tgatctgttg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320

-687-

ttgcaagacc	ggatgttcaa	atttgaactc	acccgcccgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgaacgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttccc	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 609

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 367 GCC

&lt;400&gt; 609

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccctcgc	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
agatgaccg	ccaaggctcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcccgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgaacgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttccc	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 610

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-688-

&lt;223&gt; Mutant rep DNA sequence:370 GCC

```

<400> 610
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa      480
accagcctg agctccagt ggcgtggact aatatggaac agtatttaag cgcctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaagaag      720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcgg      780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900
atthttggaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggccc      960
acgaaaaaagt tcggcaagag gaacaccatc tggtctgtttg ggcctgcaac taccgggaag      1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc      1080
aatgagaact ttcccttcaa cgactgtgcc gacaagatgg tgatctggtg ggaggagggg      1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc      1200
gtggaccaga aatgcaagtc ctcgccccag atagacccca ctcccgatgat cgtcacctcc      1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ctttcgaaca ccagcagccg      1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag      1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg      1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gacccgcccc cagtgcagca      1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg      1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg      1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc      1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt      1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg      1800
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa      1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga      1920
cactctctct ga                                     1932

```

&lt;210&gt; 611

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence:376 GCG

```

<400> 611
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctccccaaa      480
accagcctg agctccagt ggcgtggact aatatggaac agtatttaag cgcctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaagaag      720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcgg      780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900

```

-689-

atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tccggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatcgctg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgctc	tggatcatga	ctthtgggaag	1380
gtcaccaagc	aggaagtcaa	agactthtttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgtcttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 612

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 381 GCG

&lt;400&gt; 612

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctgtagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accacgcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtgc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tgggtggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tccggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
gcgatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgctc	tggatcatga	ctthtgggaag	1380
gtcaccaagc	aggaagtcaa	agactthtttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgtcttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932



-690-

<210> 613  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence:382 GCG

<400> 613  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgactttc tgacggaatg gcgcctgtg agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420  
 gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
 acccagcctg agctccagtg ggcgtggact aatatggaac agtattttaag cgcctgtttg 540  
 aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
 gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
 tcagccagggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcgagagaag 720  
 cagtggatcc aggaggacca ggccctcatac atctccttca atgcggcctc caactcgcgg 780  
 tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840  
 cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
 attttggaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggccc 960  
 acgaaaaagt tccggcaagag gaacaccatc tggctgtttg ggccctgcaac taccgggaag 1020  
 accaaccatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080  
 aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
 aaggcgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200  
 gtggaccaga aatgcaagt ctcggcccag atagaccga ctcctcgat cgtcacctcc 1260  
 aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
 ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380  
 gtcaccaagc aggaagtcaa agactttttc cggtagggcaa aggatcacgt ggttgaggtg 1440  
 gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gacccgcccc cagtgcgca 1500  
 gatataagt agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
 gaagcttca tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620  
 aatctgatgc tggttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680  
 ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccctgt 1740  
 tctgtcgtca aaaaaggcgt tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800  
 ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860  
 caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920  
 cactctctct ga 1932

<210> 614  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 389 GCG

<400> 614  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgactttc tgacggaatg gcgcctgtg agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420  
 gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
 acccagcctg agctccagtg ggcgtggact aatatggaac agtattttaag cgcctgtttg 540

-691-

aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcgggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaagggtcgt	ggaggcggcc	aaagccattc	tcggagggaag	caagggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	agctgttcaa	atttgaactc	acccgcctgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 615

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 407 GCC

&lt;400&gt; 615

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtgaagccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagatttcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaataca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcgggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaagggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caagggtgcgc	1200
gtggaccaga	aatgcaaggc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcctgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620

-692-

```

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaaga ctgttttagag tgctttcccg tgtcagaatc tcaacccggt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaagggtg 1800
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 616

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 411 GCA

&lt;400&gt; 616

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgcccgttg agtaaggccc cggaggccct tttctttgtg 240
caattttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480
accgacctg agctccaagt ggcggtgact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccagggt acatggagct ggtcgggttg ctctgtggaca aggggattac ctcggaag 720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taaacgggta cgatccccaa tatgcccgtt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctccggccag gcagaccoga ctcccgtgat cgtcacctcc 1260
aacaccaaca tqtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atthgaaatc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gacccgcccc cagtgcgcga 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtag caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaaga ctgttttagag tgctttcccg tgtcagaatc tcaacccggt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaagggtg 1800
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 617

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 414 GCT

&lt;400&gt; 617

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120

```

-693-

tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctt	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccg	atagaccccg	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaactc	acccgcgctc	tggtatcatg	ctttgggaag	1380
gtcaccaaag	aggaagtcaa	agactttttc	cggtagggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtgtgcg	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthtccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcaag	gacagaaaag	ctgttttagag	tgctttcccg	tgatcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	gtataatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 618

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 420 GCT

&lt;400&gt; 618

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gcccagaaag	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctt	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200

-694-

gtggaccaga	aatgcaagtc	ctcggcccg	atagaccgga	ctcccgtgat	cgtcaccgct	1260
aacaccaaca	tgtgcccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 619

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 421 GCC

&lt;400&gt; 619

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgaacttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagg	ggtggatgag	tgctacatcc	ccaattactt	gtcccccaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaac	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
gccaccaaca	tgtgcccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 620

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-695-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 422 GCC

&lt;400&gt; 620

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccg	atagaccgga	ctcccgtgat	cgtcacatcc	1260
aacgccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagtttcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgatcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tgatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 621

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 424 GCG

&lt;400&gt; 621

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-696-

```

ccccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taaacgggta cgatccccc aaacaccatc cggctgtttt gggatgggccc 960
acgaaaaagt tccggcaagag gaacaccatc tggctgtttt ggcttgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgctg 1200
gtggaccaga aatgcaagtc ctccggcccag atagaccgca ctcccgatg cgtcacctcc 1260
aacaccaacg cgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gacccgcccc cagtgcagca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtag agccatcgac gttctcgta cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaagggcgt tcagaaactg tgcctacatt atcatatcat gggaaagggtg 1800
ccagacgctt gactgcctg cgatctgggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 622

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 428 GCT

&lt;400&gt; 622

```

acggcggggg tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga cgtggccga gaagctgcag 180
cgcgactttc tgacgggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caattttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcgggg tcgagccgac tttgccaaac tggttcgctg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaa cagtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc agggaggacca ggccctcatc atctccttca atgcggcctc caactcgctg 780
tcccaaatca aggtgcctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840
ccccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taaacgggta cgatccccc aaacaccatc cgtctttctt gggatgggccc 960
acgaaaaagt tccggcaagag gaacaccatc tggctgtttt ggcttgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgctg 1200
gtggaccaga aatgcaagtc ctccggcccag atagaccgca ctcccgatg cgtcacctcc 1260
aacaccaaca tgtgcgccgt ggctgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gacccgcccc cagtgcagca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtag agccatcgac gttctcgta cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaagggcgt tcagaaactg tgcctacatt atcatatcat gggaaagggtg 1800
ccagacgctt gactgcctg cgatctgggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920

```

-697-

cactctctct ga

1932

&lt;210&gt; 623

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence:429 GCC

&lt;400&gt; 623

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgcccgg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccgaag	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1500
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1560
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1620
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgtgt	1680
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1740
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1800
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1860
cactctctct	ga					1920
						1932

&lt;210&gt; 624

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 438 GCG

&lt;400&gt; 624

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420



-698-

```

gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgag ggaagatta tgagcctgac taaaaccgcc 840
cccactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtgaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggac 960
acgaaaaagt tcggcaagag gaacaccatc aaagcattt ggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccag atagaccga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgcgtt gattgacggg aactcaacga ccttcgaaca cgcgcagccg 1320
ttgcaagacc ggaagtcaa atttgaactc acccgcgctc tggatcatga ctttgggaag 1380
gtcaccgaagc aggaagtcaa agacttttcc cgggtggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccggcccc cagtacgca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccctgt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 625

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 440 GCG

&lt;400&gt; 625

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcaccctga cctgaggcca gaagctgcag 180
cgcactttc tgacggaatg ggcgcgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaac tggttcgctg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgag ggaagatta tgagcctgac taaaaccgcc 840
cccactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtgaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggac 960
acgaaaaagt tcggcaagag gaacaccatc aaagcattt ggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccag atagaccga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgcgtt gattgacggg aactcaacga ccttcgaaca ccagcagggc 1320
ttgcaagacc ggaagtcaa atttgaactc acccgcgctc tggatcatga ctttgggaag 1380
gtcaccgaagc aggaagtcaa agacttttcc cgggtggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccggcccc cagtacgca 1500

```

-699-

gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 626

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 451 GCC

&lt;400&gt; 626

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttcac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgag	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcgg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gtcccccaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	cgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	gcccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gaccgcggcc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 627

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 460 GCG

&lt;400&gt; 627

-700-

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaa	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgctgcgcgt	gattgacggg	aaactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggtatcatga	ctttggggcg	1380
gtcaccgaag	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gaccgcggcc	cagtgcagca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcgatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 628

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 462 GCC

&lt;400&gt; 628

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaa	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080

-701-

aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgcgtc	tggatcatga	ctttgggaag	1380
gtcgccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaaggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 629

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 462 ATA

&lt;400&gt; 629

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctgtagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgcacgtgc	gcagacgcag	600
gagcagaaca	aaagagaatca	gaatcccaat	tctgatgcgc	cggatgcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcgcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgcgtc	tggatcatga	ctttgggaag	1380
gtcataaaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaaggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 630

&lt;211&gt; 1932

-702-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 484 GCC

&lt;400&gt; 630

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caattttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa      480
accgcgctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcgagaaag      720
cagtggatcc aggaggacca ggccctcatac atctccttca atgcggcctc caactcgcg      780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgac      840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900
attttgaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggac      960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag      1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc      1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg      1140
aagatgacct ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc      1200
gtggaccaga aatgcaagtc ctccggccag atagaccoga ctcccgtgat cgtcacctcc      1260
aacaccaaca tgtgcgcgtg gattgacggg aactcaacga ccttcgaaca ccagcagccg      1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag      1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg      1440
gagcatgaag cctactgcaa aaaggggtgga gccaaagaaa gaccgcgcc cagtgcgca      1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg      1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg      1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc      1680
ttcactcacg aacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaacccgtt      1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg      1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa      1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga      1920
cactctctct ga                                     1932

```

&lt;210&gt; 631

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 488 GCG

&lt;400&gt; 631

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg      240
caattttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa      480
accgcgctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660

```

-703-

tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccc	tatgcgggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtcggcc	aaagccattc	tcggaggaag	caagggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcccgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	accgcgctc	tggatcatga	ctthtgggaag	1380
gtcaccagac	aggaagtcaa	agactthtttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	agcgggtgga	gccaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttctga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgta	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgthtttagag	tgctthtccc	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	thtaaatcag	gtatggctgc	cgatggtht	ctccagat	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 632

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 495 GCC

&lt;400&gt; 632

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	thttgggacg	thtccctgagt	cgatttcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	togagccgac	thtgccaaac	tggttcgagg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agttattha	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccc	tatgcgggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	thccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtccggc	aaagccattc	tcggaggaag	caagggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcccgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	accgcgctc	tggatcatga	ctthtgggaag	1380
gtcaccagac	aggaagtcaa	agactthtttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gagccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttctga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgta	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgthtttagag	tgctthtccc	tgtcagaatc	tcaaccggtt	1740

-704-

tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 633  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 497 GCC

<400> 633						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	ggttggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgccgc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 634  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 497 CGA

<400> 634						
acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240

-705-

caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaaac	taaacgggta	cgatccccc	tatgcggcct	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	aagtgcgcga	1500
gatataagtg	agcccaaacc	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaaacaaat	gttctcgtca	cgtgggcattg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gcagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 635

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 497 CTC

&lt;400&gt; 635

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaaac	taaacgggta	cgatccccc	tatgcggcct	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320



-706-

ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgcgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcctc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttcctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 636

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 497 TAC

&lt;400&gt; 636

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggtgtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgacagtgct	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgctg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccggt	gaggacattt	ccagcaatcg	gattttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcgggctt	ccgtctttct	gggatggggcc	960
acgaaaaaagt	tcggcaagag	gaacaccatc	tggtcgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgcaccg	ccaaggctcg	ggagtgcggc	aaagccattc	tcggaggaag	caagggtgcg	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgctcacctcc	1260
aaacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgcgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgccta	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttcctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 637

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

-707-

&lt;223&gt; Mutant rep DNA sequence: 498 GCT

```

<400> 637
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagcttttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaac tggttcgctg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccagggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaag 720
cagtggtacc agggagacca ggcctcatal atctccttca atgcccctc caactcgcgg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccggt gaggacattt ccagcaatcg gatttataaa 900
attttggaa taaacgggta cgatcccaaa tatcggtt ccgtctttct gggatggggc 960
acgaaaaagt tccgcaagag gaacaccatc tggtctgttt ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgccccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaaagatt aaagccattc tcggagggaag 1140
aagatgaccg ccaaggtcgt ggagtgcggc aaagccattc atagaccgga ctcccgtgat 1200
gtggaccaga aatgcaagtc ctccggccag aactcaacga ccttogaaca ccagcagccg 1260
aacaccaaca tgtgcgccgt gattgacggg acccgccgtc tggatcatga ctttgggaag 1320
ttgcaagacc ggatgttcaa atttgaactc cgggtgggcaa aggatcacgt ggttgagggtg 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gaccgcgcc cgtgacgca 1500
gatataatg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc tgctttcccg tgcagaatc tcaaccggtt 1680
ttcactcacg gacagaaaga ctgttttagag gagagaatga atcagaattc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcactgcctg cgaatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat ctccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 638

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence:499 GCC

```

<400> 638
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagcttttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaac tggttcgctg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccagggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaag 720
cagtggtacc agggagacca ggcctcatal atctccttca atgcccctc caactcgcgg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccggt gaggacattt ccagcaatcg gatttataaa 900

```

-708-

atthttggaac	taaacgggta	cgatcccca	tatgcggtt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 639

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 503 GCG

&lt;400&gt; 639

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttct	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttcttttgt	240
caatttgaga	agggagagag	ctacttcac	atgcacgtgc	tcgtggaaac	caccgggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accacccctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgtactac	tggtgggcca	gcagcccgtg	gaggcaattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggtt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagcg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

-709-

<210> 640  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 510 GCA

<400> 640  
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgagg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
aatctcacgg agcgtaaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaagaag 720  
cagtggatcc agggaggacca ggcctcatat atctccttca atgcccctc caactcgagg 780  
tcccaaatca aggcctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840  
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
atthttggaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatgggccc 960  
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggccctgcaac taccgggaag 1020  
accaacatcg cggaggccat agcccacact gtgcctttct acgggtgagc aaactggacc 1080  
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctgggt ggaggagggg 1140  
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200  
gtggaccaga aatgcaagtc ctcgcccag atagaccgga ctcccgtgat cgtcacctcc 1260  
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
ttgcaagacc ggatgttcaa atthgaactc acccgccgtc tggatcatga ctttgggaag 1380  
gtcaccgaagc aggaagtcaa agacttttct cgggtgggcaa aggatcacgt ggttgaggtg 1440  
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcgcc cagtgacgca 1500  
gatataagtg agcccaaacg ggtgcgcgca tcagttgcgc agccatcgac gtcagacgcg 1560  
gaagcttcga tcaactacgc agacaggtag caaaacaaat gttctcgtca cgtgggcatg 1620  
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaatc aaatatctgc 1680  
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggt 1740  
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggtg 1800  
ccagacgctt gcactgcctg cgatctgggt aatgtggatt tggatgactg catctttgaa 1860  
caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

<210> 641  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 511 GCA

<400> 641  
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgagg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540

-710-

aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgtactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtgggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacatc	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	gcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagagcgtt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 642

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 512 GCT

&lt;400&gt; 642

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgacttct	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgtactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtgggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacatc	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagctgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620

-711-

```

aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcaactgcctg cgatctgggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatgggtgc cgatgggtat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

```

<210> 643
<211> 1932
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep DNA sequence: 516 GCG

```

```

<400> 643
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc . 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatattggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaagaa 720
cagtggatcc agggagacca ggctcatcac atctccttca atgcggcctc caactcgcgg 780
tcccaaatca aggtgcctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840
cccactacc tgggtggcca gcagcccggtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taaacgggtg cgatcccaaa tatgcggctt ccgtctttct gggatggggc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctggcccgag atagaccgca ctcccgatgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc accgcgcgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agacttttcc cgggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcgcc cagtgcgca 1500
gatataagt agcccaaacg ggtgcgcgag tcagttgcgc agccagcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcaactgcctg cgatctgggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatgggtgc cgatgggtat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

```

<210> 644
<211> 1932
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Mutant rep DNA sequence: 517 GCT

```

```

<400> 644
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120

```

-712-

tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccaga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	accgcgcgtc	tggatcatga	ctttgggaa	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgcc	ttcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggatc	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatcg	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	cgactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 645

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 517 AAC

&lt;400&gt; 645

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200

-713-

gtggaccaga	aatgcaagtc	ctcggccccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcccgcg	tcagttgcgc	agccatcgaa	ctcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 646

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 518 GCA

&lt;400&gt; 646

acggcgggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaattccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaa	taaacgggta	cgatcccca	tatgcccgtt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caagggtgcg	1200
gtggaccaga	aatgcaagtc	ctcggccccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcccgcg	tcagttgcgc	agccatcgac	ggcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 647

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



-714-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 519 GCG

&lt;400&gt; 647

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccaaa	tatgcggcct	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggccag	atagaccga	ctcccgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atltgaaact	acccgcctgc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataaagt	agcccaaacg	ggtgcgcgag	tcagtgcgc	agccatcgac	gtcagcggcg	1560
gaagcttcca	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcagc	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tgatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 648

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 598 GCA

&lt;400&gt; 648

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-715-

cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gaccgcggcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgcgtt	1740
tctgtcgtca	aaaagggcgt	tcagaaactg	tgctacattc	atcatatcat	ggcaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 649

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 600 GCG

&lt;400&gt; 649

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcgagagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgccg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gaccgcggcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgcgtt	1740
tctgtcgtca	aaaagggcgt	tcagaaactg	tgctacattc	atcatatcat	gggaaaggcg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920

-716-

cactctctct ga

1932

<210> 650  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 601 GCA

<400> 650  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420  
 gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
 acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
 aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
 gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
 tcagccaggt acatggagct ggtcgggtgg ctcggtggaca aggggattac ctgggagaag 720  
 cagtggatcc aggaggacca ggccctcatc atctccttca atgcggcctc caactcgcgg 780  
 tcccaaatca aggtgcctt ggacaatgag ggaagatta tgagcctgac taaaaccgcc 840  
 cccgactacc tgggtgggcca gcagcccgtg gaggcattt ccagcaatcg gatttataaa 900  
 attttggaac taaacgggta cgatcccaaa tatgcggcct ccgtctttct gggatgggccc 960  
 acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggccctgcaac taccgggaag 1020  
 accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080  
 aatgagaact ttoccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
 aagatgaccg ccaaggctcg ggagtgcggc aaagccattc tcggaggaag caaggtgcgc 1200  
 gtggaccaga aatgcaagtc ctccggccag atagaccgga ctcccgtgat cgtcacctcc 1260  
 aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
 ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380  
 gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg 1440  
 gagcataaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcgcc cagtgcgcg 1500  
 gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
 gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620  
 aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680  
 ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccgctt 1740  
 tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800  
 gcagacgctt gcaactgcct cgatctggtc aatgtggatt tggatgactg catctttgaa 1860  
 caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920  
 cactctctct ga 1932

<210> 651  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 335 420, 495 GCT GCC GCC

<400> 651  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420

-717-

```

gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccactacc tgggtgggcca gcagcccggt gaggaacatt ccagcaatcg gatttataaa 900
atthtgggaa taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatggggc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg gggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtgcggc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctccggccag atagacccga ctcccgatg cgtcaccgcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atthgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccgaag aggaagtcaa agacttttct cgggtggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaaggttggg gccaaagaaa gagccgcccc cagtacgcga 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtag caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaatc aaatatctgc 1680
ttcactcacg gacagaaaga ctgtttagag tgctttcccg tgtcagaatc tcaaccggt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt cagctgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 652

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 39 140 GCA GCC

&lt;400&gt; 652

```

acggcggggg tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgcgagat 120
tctgacatgg atctgaatct gattgagcag gcacccttga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttcac atgcacgtgc tcgtggaaac caccgggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcgggg tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatgcc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaagaag 720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccactacc tgggtgggcca gcagcccggt gaggaacatt ccagcaatcg gatttataaa 900
atthtgggaa taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatggggc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtgcggc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctccggccag atagacccga ctcccgatg cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atthgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccgaag aggaagtcaa agacttttct cgggtggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaaggttggg gccaaagaaa gaccgcccc cagtacgcga 1500

```

-718-

gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttccctg	cagacaatgc	gagagaatga	atcagaatcc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 653

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 279 428 451 GCC GCT GCC

&lt;400&gt; 653

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	tggttcgcgg	tcacaaagac	tcagagaatt	360
taccgcgggga	tcgagccgac	tttgccaaac	tgctacatcc	ccaattactt	gctccccaaa	420
gccggaggcg	ggaacaagggt	gggtggatgag	aatatggaac	agtatattaag	cgctgtttg	480
acccagcctg	agctccagtg	ggcgtggact	cagcatctga	cgacagtgtc	gcagacgcag	540
aatctcacgg	agcgtaaacg	ggttgggtggc	tctgatgcgc	cggtgatcag	atcaaaaact	600
gagcagaaca	aagagaatca	gaatcccaat	ctcgtggaca	aggggattac	ctcggagaag	660
tcagccaggt	acatggagct	ggtcgggtg	atctccttca	atgcggcctc	caactcgcg	720
cagtggatcc	aggaggacca	ggcctcatac	ggaaagatta	tgagcctgac	taaagccgcc	780
tcccaaatca	aggctgcctt	ggacaatgcg	gaggacattt	ccagcaatcg	gatttataaa	840
cccgaactacc	tggtgggcca	gcagcccgtg	tatgcggtct	ccgtctttct	gggatgggccc	900
attttggaac	taaacgggta	cgatccccaa	tggtctgtttg	ggcctgcaac	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	gtgcccttct	acgggtgctg	aaactggacc	1020
accaacatcg	cggaggccat	agccacact	gacaagatgg	tgatctggtg	ggaggagggg	1080
aatgagaact	ttcccttcaa	cgactgtgtc	aaagccattc	tcggaggaag	caaggtgcgc	1140
aagatgaccg	ccaaggtcgt	ggagtggccc	atagaccgca	ctcccgtgat	cgtcacctcc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	aactcaacga	ccttcgaaca	ccagcagccg	1260
aacaccaaca	tgtgcgccgt	ggctgacggg	gcccgcgctc	tggtatcatga	ctttgggaag	1320
ttgcaagacc	ggatgttcaa	atttgaactc	cggtgggcaa	aggatcacgt	ggttgaggtg	1380
gtcaccaagc	aggaagtcaa	agactttttc	gccaagaaaa	gacccgcccc	cagtgcagca	1440
gagcatgaat	tctactgcaa	aaaggggtgga	tcagttgcgc	agccatcgac	gtcagacgcg	1500
gatataagtg	agcccaaacg	ggtgcgcgag	caaaacaaat	gttctcgtca	cgtgggcatg	1560
gaagcttcga	tcaactacgc	agacagggtac	gagagaatga	atcagaatcc	aaatatctgc	1620
aatctgatgc	tgttccctg	cagacaatgc	tgctttcccg	tgtcagaatc	tcaaccggtt	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctacattc	atcatatcat	gggaaagggtg	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	aatgtggatt	tggtgactg	catctttgaa	1800
ccagacgctt	gcactgcctg	cgatctgggtc	cgatggttat	cttccagatt	ggctcgagga	1860
caataaatga	tttaaatcag	gtatggctgc				1920
cactctctct	ga					1932

&lt;210&gt; 654

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 125 237 600 GCG GCC GCG

&lt;400&gt; 654

-719-

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttcac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgcgccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatcgcg cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattgc ctcggaag 720
cagtggtacc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccgag atagaccga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atthtgaact acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agacttttct cggtagggca aggatcacgt ggttaggtg 1440
gagcatgaat tctacgtcaa aaaggggtgga gccaaagaaa gaccgcgcc cagtgcagca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcca tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtta aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaggcg 1800
ccagacgctt gcactgcctg cgatctgggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 655

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 163 259 GCT GCG

&lt;400&gt; 655

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttcac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatcgcg cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaag 720
cagtggtacc aggaggacca ggcctcatat atctccttca atgcggcctc caacgcgcgg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthttggaac taacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080

```

-720-

aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcggt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 656

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 17 127 189 GCG GCT GCG

&lt;400&gt; 656

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacgc	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcgctgtg	agtaaggccc	cggaggccct	ttcttttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgag	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	ggtggcggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgacag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcggt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 657

&lt;211&gt; 1932

-721-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 428 GCT GCT

&lt;400&gt; 657

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccaagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacgct	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	ggctgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgaacga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgag	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcagc	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 658

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 338 495 GCC GCC GCC

&lt;400&gt; 658

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccaagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660



-722-

tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	tgccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaact	acccgcctgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gagccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaagggcga	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 659

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 350 420 GCT GCC

&lt;400&gt; 659

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgcctgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cgatttcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	gggtgatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacgct	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacccgc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaact	acccgcctgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740

-723-

tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 660  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 189 197 518 GCG GCG GCA

<400> 660						
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttggcggcg	cagcatctga	cgcacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaaac	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gaccgcgcc	cagtgaacga	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	ggcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 661  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 468 516 GCC GCG

<400> 661						
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240

-724-

caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgacagtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tgatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agcctttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccagcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgt	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 662

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 127 221 350 54 140 GCT

GCA GCT GCC GCC

&lt;400&gt; 662

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgacagtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
gcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacgtc	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260

-725-

aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 663

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 285 GCA GCG

&lt;400&gt; 663

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatct	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	gggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgccctgttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
gcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggcggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgttg	ggaggagggtg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagt	ctcggcccag	atagaccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 664

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-726-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 23 495 GCT GCC

&lt;400&gt; 664

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcatttgctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccctcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccacagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gatataagtg	agcccaaacg	ggtgcgcgag	gccaagaaaa	gagccgcccc	cagtgcgcga	1500
gaagcttcga	tcaactacgc	agacaggtac	tcagttgcgc	agccatcgac	gtcagacgcg	1560
aatctgatgc	tgtttccctg	cagacaatgc	caaaacaaat	gttctcgtca	cgtgggcatg	1620
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	aaatatctgc	1680
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 665

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mutant rep DNA sequence: 20 54 420 495 GCC GCC GCC  
GCC

&lt;400&gt; 665

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780

-727-

tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcaccgcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcccgtc	tggatcatga	ctttgggaag	1380
gtcaccagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gagccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 666

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 412 612 GCC GCG

&lt;400&gt; 666

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagcccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcccgtc	tggatcatga	ctttgggaag	1380
gtcaccagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gaccgcgccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgcggatt	tggatgactg	catctttgaa	1860

-728-

caataaatga tttaaatacag gtatggctgc cgatgggttat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

<210> 667  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 197 412 GCG GCC

<400> 667  
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgcccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480  
accagcctg agctccagt ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtggc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcgagaaag 720  
cagtggatcc aggaggacca ggccctcatc atctccttca atgcggcctc caactcgcgg 780  
tcccaaatca aggtctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840  
cccgaactac tggtagggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
atthttggaac taaacgggta cgatccccaat tatgcccgtt ccgtctttct gggatggggc 960  
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020  
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080  
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200  
tgggaccaga aatgcaagtc ctcgcccgag atagcccga ctcccgtgat cgtcacctcc 1260  
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
ttgcaagacc ggatgttcaa atthgaactc acccgccgtc tggatcatga ctttgggaag 1380  
gtcaccaagc aggaagtcaa agactttttc cggtagggcaa aggatcacgt ggttaggtg 1440  
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcccc cagtgcgca 1500  
gatataagt agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620  
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680  
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740  
tctgtcgtca aaaaggcgtg tcagaaactg tgctacatc atcatatcat gggaaaagtg 1800  
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860  
caataaatga tttaaatacag gtatggctgc cgatgggttat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

<210> 668  
<211> 1932  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Mutant rep DNA sequence: 412 495 511 GCC GCC GCA

<400> 668  
acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgcccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360

-729-

taccgcgggga	tgcagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctcg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatal	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctt	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagccccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gagccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	gcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgcgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 669

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 98 422 GCC GCC

&lt;400&gt; 669

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	cgccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagatttcgcg	aaaaactgat	tcagagaatt	360
taccgcgggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctcg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatal	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctt	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgtgat	cgtcacctcc	1260
aacgccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440



-730-

gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcacgca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 670

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 17 127 189 GCG GCT GCG

&lt;400&gt; 670

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacgc	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtattttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggcggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcccctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcgcccgag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggttgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcacgca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 671

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 20 54 495 GCC GCC GCC

-731-

```

<400> 671
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctggcc 60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctgg ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttgggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcgagaag 720
cagtggatcc aggaggacca ggcctcctac atctccttca atgcggcctc caactcgcgg 780
tcccaaatca aggtgcctt ggacaatcgc ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtggaaac taaacgggta cgatcccaaa tatgcccgtt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctgggt ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200
gtggaccaga aatgcaagt ctcggcccag gattgacggg acccgccgtc tggatcatga ctttgggaag 1380
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cggtgggcaa aggatcacgt ggttgagggt 1440
gagcataaat tctacgtcaa aaagggtgga gccaaagaaa gagccgcccc cagtacgca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaaaggtg 1800
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga gtaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 672

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 163 GCC GCT

```

<400> 672
acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctgg ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttgggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctcgtggaca aggggattac ctcgagaag 720
cagtggatcc aggaggacca ggcctcctac atctccttca atgcggcctc caactcgcgg 780
tcccaaatca aggtgcctt ggacaatcgc ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtggaaac taaacgggta cgatcccaaa tatgcccgtt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020

```

-732-

accaa	catcg	cggaggccat	agcccacact	gtgcccttct	acgggtg	gcgt	aaactggacc	1080
aatgaga	aact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagg	ggaggagg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtg	gcgc	caaggtg	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc		cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg		ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag		ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg		ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga		cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg		gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg		cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc		aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt		tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg		gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa		catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga		ggctcgagga	1920
cactctctct	ga							1932

&lt;210&gt; 673

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 259 54 GCG GCC

&lt;400&gt; 673

acggcg	gggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60	
ggcatttctg	acagctttgt	gaactgggtg	gcccagagaagg	aatgggagtt	gccgccagat		120	
tctgacatgg	atctgaatct	gattgagcag	gcaccccttg	cgtggccga	gaagctgcag		180	
cgcgactttc	tgacggaatg	gcgcgctgtg	agtaaggccc	cggaggccct	tttctttgtg		240	
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	cacgggggtg		300	
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt		360	
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc		420	
gccggaggcg	ggaacaaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa		480	
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg		540	
aatctcacgg	agcgtaaaacg	gttgggtggc	cagcatctga	cgacacgtgc	gcagacgcag		600	
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact		660	
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag		720	
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caacgcgcgg		780	
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc		840	
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa		900	
atthttggaac	taaacgggta	cgatcccaa	tatgcggctt	ccgtctttct	gggatgggccc		960	
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtttg	ggcctgcaac	taccgggaag		1020	
accaa	catcg	cggaggccat	agcccacact	gtgcccttct	acgggtg	gcgt	aaactggacc	1080
aatgaga	aact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagg	ggaggagg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtg	gcgc	caaggtg	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc		cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg		ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag		ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg		ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga		cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg		gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg		cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc		aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt		tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg		gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa		catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga		ggctcgagga	1920
cactctctct	ga							1932

&lt;210&gt; 674

-733-

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 335 399 GCT GCG

&lt;400&gt; 674

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa      480
accagcctg agctccagt ggctgggact aatatggaac agtatttaag cgctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact      660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggagaag      720
cagtggtatcc aggaggacca ggccctcatac atctccttca atgcggcctc caactcgcg      780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc      840
cccgaactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa      900
atthtggaaac taaacgggta cgatcccaaa tatgcggctt ccgtctttct gggatggggc      960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg gggctgcaac taccgggaag      1020
accaacatcg cggaggccat agccacact gtgccttct acgggtgcgt aaactggacc      1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctgggt ggaggagggg      1140
aagatgaccg ccaaggtcgt ggagtgcggc aaagccattc tcggagggaag caaggcgcg      1200
gtggaccaga aatgcaagtc ctgcggccag atagaccgga ctcccgatg cgtcacctcc      1260
aacaccaaca tgtgcgcgt gattgacggg aactcaacga ccttcgaaca ccagcagccg      1320
ttgcaagacc ggatgttcaa atthgaactc accgcgcgtc tggatcatga ctttgggaag      1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg      1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcgcc cagtgcgca      1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg      1560
gaagcttcga tcaactacgc agacaggtag caaaacaaat gttctcgtca cgtgggcatg      1620
aatctgatgc tgtttccctg cagacaatgc ctgttttagag tgctttcccg tgtcagaatc tcaaccggt      1680
ttactcacg gacgaaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggt      1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggt      1800
ccagacgctt gactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa      1860
caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga      1920
cactctctct ga                                     1932

```

&lt;210&gt; 675

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 432 GCA GCA

&lt;400&gt; 675

```

acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc      60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat      120
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag      180
cgcgactttc tgacggaatg gcgcccgtgt agtaaggccc cggaggccct tttctttgtg      240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg      300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt      360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc      420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa      480
accagcctg agctccagt ggctgggact aatatggaac agtatttaag cgctgtttg      540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag      600

```

-734-

gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
gcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcy	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atatttgaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tccgcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tccgaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aacgcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcctg	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggatgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcagc	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 676

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 259 516 GCG GCG

&lt;400&gt; 676

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcatcttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaattccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caacgcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcy	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atatttgaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tccgcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tccgaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcctg	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggatgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccagcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680

-735-

ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 677  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 495 516 GCC GCG

<400> 677						60
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	120
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	180
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	240
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	300
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	360
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	420
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	480
gccggaggcg	ggaacaagggt	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	540
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	600
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	660
gagcagaaca	aagagaatca	gaatcccaat	tctgatcgcg	cggtgatcag	atcaaaaact	720
tcagccagggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	780
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgagg	840
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	900
cccgaactac	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	960
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	1020
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttt	ggcctgcaac	taccgggaag	1080
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1140
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1200
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1260
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtaacctcc	1320
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1380
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgcgt	tggtatcatga	ctttgggaag	1440
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1500
gagcatgaat	tctacgtcaa	aaaggggtga	gccaagaaaa	gagccgcccc	cagtgcgcga	1560
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccagcgac	gtcagacgcg	1620
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1680
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1740
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1800
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1860
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1920
caataaatga	tttaaatacag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1932
cactctctct	ga					

<210> 678  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 414 14 GCT GCC

<400> 678						60
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	cccttgacga	gcatctgccc	120
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	180
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	

-736-

cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgctg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
aattgggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccccg	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcctgc	tggtatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcacgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactcg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt.	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 679

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 74 402 495 GCG GCC GCC

&lt;400&gt; 679

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccg	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttctctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgctg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
aattgggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggcccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgtgat	cgtcacctcc	1260

-737-

aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gagccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 680

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 228 462 497 GCC GCC GCC

&lt;400&gt; 680

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattccgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtattttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggccgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaaac	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaaactcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcgccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 681

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



-738-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 290 338 GCG GCC

&lt;400&gt; 681

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggaatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtgggcca	gcagcccgcg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	tgccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagt	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagagcccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctactgcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaaactg	tgctacattc	atcatatcat	gggaaaagtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 682

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 140 511 GCC GCA

&lt;400&gt; 682

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-739-

```

cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
attttggaaac taaacgggta cgatcccca tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcttgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccag atagaccgga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga cttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gacccgcccc cagtgcgca 1500
gatataagtg agcccaaacg ggtgcgcgag gcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga

```

&lt;210&gt; 683

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 86 378 GCG GCG

&lt;400&gt; 683

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgacgag gcacccttga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgcggtgtg agtaaggccc cggaggccct tttctttgtg 240
caattttgaga agggagcagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
accgacgtg agctccagtg ggctggact aatatggaac agtatttaag cgcctgtttg 540
aatctcacgg agcgtaaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgtgaca aggggattac ctcgagaag 720
cagtggtacc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcgg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
attttggaaac taaacgggta cgatcccca tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcttgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgctg aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccag atagaccgga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga cttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gacccgcccc cagtgcgca 1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920

```

-740-

cactctctct ga

1932

<210> 684  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 54 86 GCC GCG

<400> 684  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctgg ccgtggccga gaagctgcag 180  
 cgcgacttct tgacggaatg gcgcccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagcgag ctacttccac atgcacgtgc tctggaagac caccggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420  
 gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480  
 acccagcctg agctccagt ggcgtggact aatatggaac agtatttaag cgcctgtttg 540  
 aatctcacgg agcgtaaacg gttgggtggc cagcatctga cgcacgtgtc gcagacgcag 600  
 gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
 tcagccaggt acatggagct ggtcgggtgg ctctgtggaca aggggattac ctcggaag 720  
 cagtggatcc agggagacca ggcctcatal atctccttca atgcggcctc caactcgcg 780  
 tcccaaatca aggtgcctt ggacaatcgc ggaaagatta tgagcctgac taaaaccgcc 840  
 cccgactacc tgggtggcca gcagcccggt gaggacattt ccagcaatcg gatttataaa 900  
 attttggaaac taaacgggta cgatcccaa tatgcccgtt ccgtctttct gggatgggcc 960  
 acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020  
 accaaccatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080  
 aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
 aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200  
 gtggaccaga aatgcaagtc ctccggccag atagaccgca ctcccgtgat cgtcacctcc 1260  
 aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
 ttgcaagacc ggatgttcaa atttgaatc acccgccgtc tggatcatga ctttgggaag 1380  
 gtcaccaagc aggaagtcaa agacttttct cgggtgggcaa aggatcacgt ggttgagggtg 1440  
 gagcatgaat tctacgtcaa aaaggtgga gccaaagaaa gacccgcccc cagtgcgca 1500  
 gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
 gaagcttctga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620  
 aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaatc aaatatctgc 1680  
 ttactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740  
 tctgtcgtca aaaaggcgta tcagaaatg tgctacattc atcatatcat gggaaagggtg 1800  
 ccagacgctt gcaactgcgt cgatctggtc aatgtggatt tggatgactg catctttgaa 1860  
 caataaatga ttttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920  
 cactctctct ga 1932

<210> 685  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 214 495 140 GCG GCC GCC

<400> 685  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgacttct tgacggaatg gcgcccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag ctacttccac atgcacgtgc tctggaagac caccggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420

-741-

```

gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtattttaag cgctgttttg 540
aatctcacgg agcgtaaacg gttgggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaaact 660
tcagccaggt acatggagct ggtcgggttg ctctgtggaca aggggattac ctcgagagaag 720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
attttgaac taaacgggta cgatcccaa tatgcggctt cgtcttttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccag atagaccoga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc accgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agacttttct cgggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaaggggtga gccaaagaaa gagccgcccc cagtgcgcga 1500
gatataagt agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggt 1740
tctgtcgtca aaaaggcgta tcagaaactg cgtacattc atcatatcat gggaaaggtg 1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga

```

&lt;210&gt; 686

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 495 511 GCC GCA

&lt;400&gt; 686

```

acggcggggg tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattgcgc aaaaactgat tcagagaatt 360
taccgcgggg tcgagccgac ttgccaac ttggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480
acccagcctg agctccagtg ggcgtggact aatatggaac agtattttaag cgctgttttg 540
aatctcacgg agcgtaaacg gttgggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaaact 660
tcagccaggt acatggagct ggtcgggttg ctctgtggaca aggggattac ctcgagagaag 720
cagtggatcc aggaggacca ggcctcatat atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggtgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
attttgaac taaacgggta cgatcccaa tatgcggctt cgtcttttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgcccag atagaccoga ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
ttgcaagacc ggatgttcaa atttgaactc accgccgtc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agacttttct cgggtgggcaa aggatcacgt ggttgaggtg 1440
gagcatgaat tctacgtcaa aaaggggtga gccaaagaaa gagccgcccc cagtgcgcga 1500

```

-742-

gatataagtg	agcccaaacg	ggtgcgcgag	gcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 687

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 495 54 GCC GCC

&lt;400&gt; 687

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactgccc	60
ggcatttctg	acagcttctg	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgacttct	tgacggaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctctgag	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	ttaaagggtg	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	gcactgtgtc	gacaagatgg	tgatctggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaact	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccgaag	aggaagtcaa	agacttttct	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gagccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 688

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 495 GCG GCC

&lt;400&gt; 688

-743-

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtggc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaag 720
cagtggtacc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg 780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtggaaac taaacgggta cgatccccaat tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080
aatgagaact ttccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140
aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggagggaag caaggtgcgc 1200
gtggaccaga aatgcaagtc ctcgccccag atagacccca ctcccgtgat cgtcacctcc 1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320
gatataagtg agcccaaacg gttgcgcgag tcagttgcgc tggatcatga ctttgggaag 1380
gtcaccaagc aggaagtcaa agacttttct cgggtgggcaa aggatcacgt ggttgagggtg 1440
gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gagccgcccc cagtgaagca 1500
gatataagtg agcccaaacg gttgcgcgag agccatcgac gtcagacgcg gtcagacgcg 1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc 1680
ttcactcacg gacagaaaaga ctgttttaga tgctttcccg tgtcagaatc tcaaccggtt 1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800
ccagacgctt gcaactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920
cactctctct ga 1932

```

&lt;210&gt; 689

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 261 20 GCC GCC

&lt;400&gt; 689

```

acggcgggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctggcc 60
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360
taccgcggga tcgagccgac tttgccaaac tgggttcgcg tcacaaagac cagaaatggc 420
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660
tcagccaggt acatggagct ggtcgggtgg ctctgggaca aggggattac ctcggaag 720
cagtggtacc aggaggacca ggcctcatal atctccttca atgcggcctc caactcgcg 780
gcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc 840
cccgactacc tgggtgggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900
atthtggaaac taaacgggta cgatccccaat tatgcggctt ccgtctttct gggatgggcc 960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020
accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc 1080

```

-744-

aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	at ttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 690

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 20 GCC GCC

&lt;400&gt; 690

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctggcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacagtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgtgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgccg	780
tcccaaatca	aggtgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaaccgc	840
cccgactacc	tggtggggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
at tttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggagcccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	at ttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 691

&lt;211&gt; 1932

-745-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 420 GCG GCC

&lt;400&gt; 691

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgtgat	cgtcaccgcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atltgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcaactcag	gacagaaaga	tgctttcccg	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 692

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 338 495 GCC GCC GCC

&lt;400&gt; 692

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660



-746-

tcagccaggt	acatggagct	ggtcgggttg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	tgccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgcgt	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	gggtgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gagccgcccc	cagtgcgcga	1500
gataataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgtttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
ctctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 693

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 427 GCG GCG

&lt;400&gt; 693

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gatttgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgaacttc	tcagcgaatg	gcgcgctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggttg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgc	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgcgt	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	gggtgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcgcga	1500
gataataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgtttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740

-747-

tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 694  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 54 228 370 387 GCC GCC  
 GCC GCG

<400> 694						60
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	120
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	180
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	240
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	300
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	360
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	420
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	480
gccggaggcg	ggaacaagggt	gggtgatgag	tgctacatcc	ccaattactt	gctcccaaaa	540
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	600
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgacagtgct	gcagacgcag	660
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	720
tcagccaggt	acatgggagct	ggccgggtgg	ctcgtggaca	aggggattac	ctcggagaag	780
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgctg	840
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	900
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	960
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	1020
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgttg	ggcctgcaac	taccgggaag	1080
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1140
aatgagaact	ttcccttcaa	cgactgtgcc	gacaagatgg	tgatctggtg	ggaggagggg	1200
aagatgaccg	ccaaggctgc	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1260
gtggaccaga	atgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1320
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1380
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1440
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1500
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcagca	1560
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1620
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1680
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1740
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1800
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1860
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1920
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1932
cactctctct	ga					

<210> 695  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 221 289 GCA GCC

<400> 695						60
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	120
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	180
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	

-748-

cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgctc	cggatgatcag	atcaaaaact	660
gcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcaggccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaaacgggt	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgcgtc	tgatcatga	ctttgggaag	1380
gtcaccagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtgtgcg	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttacttcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tgatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 696

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 163 GCC GCT

&lt;400&gt; 696

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccaggctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgctc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggaatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaaacgggt	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260

-749-

aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttggggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcacgca	1500
gatataagtg	agcccaaacy	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 697

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 341 407 420 GCC GCC GCC

&lt;400&gt; 697

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgag	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgagg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaaac	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatgag	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccggggaag	1020
gccaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaaggc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcaccgcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttggggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcccc	cagtgcacgca	1500
gatataagtg	agcccaaacy	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 698

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

-750-

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 54 228 GCC GCC

&lt;400&gt; 698

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctgg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tgggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggccgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcccctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcggt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccaaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gatataagtg	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgca	1500
gaagcttcga	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
aatctgatgc	tgtttccctg	agacagggtac	caaaacaaat	gttctcgta	cgtgggcatg	1620
ttcactcacg	gacagaaaga	cagacaatgc	tgctttcccg	atcagaattc	aaatatctgc	1680
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1740
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1800
caataaatga	tttaaatcag	gtatggctgc	cgatgggttat	cttcagatt	ggctcgagga	1860
cactctctct	ga					1920
						1932

&lt;210&gt; 699

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 96 125 511 GCA GCG GCA

&lt;400&gt; 699

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggcaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tgggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcccctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840

-751-

cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcccgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gaccgcgccc	cagtgcagca	1500
gatataagt	agcccaaacg	ggtgcgcgag	gcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 700

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 420 GCG GCC

&lt;400&gt; 700

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gatttgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacgggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaa	agtatthtaag	cgctgtttg	540
aatctcacgg	agcgtaaaacg	gttggtggcg	cagcatctga	cgcacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggtatcc	aggaggacca	ggcctcatatc	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgatg	cgtcaccgcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcccgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gaccgcgccc	cagtgcagca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920

-752-

cactctctct ga

1932

&lt;210&gt; 701

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 334 428 499 GCG GCT GCC

&lt;400&gt; 701

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagt	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatal	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaaacgggtg	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	cgcttgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcgggcccg	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	ggctgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcggtc	tggtatcatga	ctttgggaag	1380
gtcaccgaagc	aggaaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gaccgcgcc	cagtgccgca	1500
gatataagt	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgctcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 702

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 197 414 GCG GCT

&lt;400&gt; 702

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	aggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420

-753-

gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgacgtggc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccaaa	tatgcccgtt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtccggc	aaagccattc	tcggaggaag	caagggtgcg	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccggg	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaactc	acccgccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aaaaggtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthtccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttactctacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 703

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 30 54 127 GCG GCC GCT

&lt;400&gt; 703

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggcg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctggg	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cgatttcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccggc	tttgccaaac	tggttcgagg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgacgtgtgc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	taaacgggta	cgatcccaaa	tatgcccgtt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggaggaag	caagggtgcg	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthgaactc	acccgccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaagaaaa	gacccgcccc	cagtgcagca	1500



-754-

gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttcctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 704

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 29 260 GCG GCG

&lt;400&gt; 704

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaacgcggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttcac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttccctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatattaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcggcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggpc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtgcggc	aaagccattc	tcggaggaag	caagggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gaccgcgcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttcctcg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccggt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 705

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 29 260 GCG GCG

&lt;400&gt; 705

-755-

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaacgcggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atlttgggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgatg	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atlttgaaact	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtggggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctactgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagtctgcg	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgcttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatgggtgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 706

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 4 484 GCT GCC

&lt;400&gt; 706

acggcggggg	cttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atlttgggaac	taaacgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080

-756-

aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaag	cctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacy	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 707

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 258 124 132 GCC GCC GCC

&lt;400&gt; 707

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccttga	ccgtggccga	gaagctgcag	180
cgcgactttc	tcagcgaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcgggg	ccgagccgac	tttgccaaac	tgggcccggg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctctgttg	540
aatctcacgg	agcgtaaaacg	ggtgggtggc	cagcatctga	cgacagtgct	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcctac	atctccttca	atgcggcctc	cgctcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tgggtggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggaggggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacy	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 708

&lt;211&gt; 1932

-757-

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 231 497 GCC GCC

&lt;400&gt; 708

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatgggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	gccgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactac	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttgggaa	taaacgggta	cgatcccaa	tatcgggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacatc	gtgcctttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggt	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgct	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atgtgaactc	acccgcgctc	tggatcatga	ctttgggaag	1380
gtcaccagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtga	gccaaagaaa	gacccgcgcg	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 709

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 221 258 GCA GCC

&lt;400&gt; 709

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatgggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660

-758-

```

gcagccaggt  acatggagct  ggtcgggtgg  ctctgggaca  aggggattac  ctcggaagaag  720
cagtggatcc  aggaggacca  ggcctcatat  atctccttca  atgcggcctc  cgcctcgagg  780
tccc aaatca  aggtgcctt  ggacaatgag  ggaaagatta  tgagcctgac  taaaaccgcc  840
cccgaactacc  tgggtgggcca  gcagcccgtg  gaggacattt  ccagcaatcg  gatttataaa  900
atthttggaac  taaacgggta  cgatcccaaa  tatgcggctt  ccgtctttct  gggatgggccc  960
acgaaaaagt  tcggcaagag  gaacaccatc  tggctgtttg  ggcctgcaac  taccgggaag  1020
accaacatcg  cggaggccat  agcccacact  gtgcccttct  acgggtgctg  aaactggacc  1080
aatgagaact  ttcccttcaa  cgactgtgtc  gacaagatgg  tgatctggtg  ggaggagggg  1140
aagatgaccg  ccaaggctcg  ggagtcggcc  aaagccattc  tcggagggaag  caaggtgctg  1200
gtggaccaga  aatgcaagtc  ctgggcccag  atagaccgga  ctcccgatg  cgtcacctcc  1260
aacaccaaca  tgtgcccgt  gattgacggg  aactcaacga  ccttcgaaca  ccagcagccg  1320
ttgcaagacc  ggatgttcaa  atthgaactc  accgcgcgtc  tggatcatga  ctttgggaag  1380
gtcaccgaag  aggaagtcaa  agactttttc  cgggtgggcaa  aggatcacgt  ggttgagggtg  1440
gagcatgaat  tctacgtcaa  aaagggtgga  gccaaagaaa  gaccgcggcc  cagtgcagca  1500
gatataagtg  agcccaaacg  ggtgcgcgag  tcagttgcgc  agccatcgac  gtcagacgag  1560
gaagcttcga  tcaactacgc  agacaggtac  caaaacaaat  gttctcgta  cgtgggcatg  1620
aatctgatgc  tgtttccctg  cagacaatgc  gagagaatga  atcagaatc  aaatatctgc  1680
ttcactcacg  gacagaaaga  ctgttttag  tgctttcccg  tgtcagaatc  tcaaccggt  1740
tctgtcgtca  aaaaggcgta  tcagaaactg  tgcataatc  atcatatcat  gggaagggtg  1800
ccagacgctt  gcactgcctg  cgatctggtc  aatgtggatt  tggatgactg  catctttgaa  1860
caataaatga  tttaaatcag  gtatgggtgc  cgatggttat  cttccagatt  ggctcgagga  1920
cactctctct  ga  1932

```

&lt;210&gt; 710

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 234 264 326 GCG GCG GCC

&lt;400&gt; 710

```

acggcgggggt  tttacgagat  tgtgattaag  gtccccagcg  accttgacga  gcatctgccc  60
ggcattttctg  acagctttgt  gaactgggtg  gccgagaagg  aatgggagtt  gccgcagat  120
tctgacatgg  atctgaatct  gattgagcag  gcaccctga  cgtggccga  gaagctgcag  180
cgcgactttc  tgacgggaatg  gcgcccgtgt  gctaaaggccc  cggaggccct  tttctttgtg  240
caatttgaga  agggagagag  ctacttccac  atgcacgtgc  tctgggaaac  caccgggggtg  300
aaatccatgg  ttttgggacg  tttcctgagt  cagattcgcg  aaaaactgat  tcagagaatt  360
taccgcggga  tcgagccgac  tttgccaaac  tggttcgagg  tcacaaagac  cagaaatggc  420
gccggagggg  ggaacaagg  ggtggatgag  tgctacatcc  ccaattactt  gctcccaaaa  480
acccagcctg  agctccagtg  ggcgtggact  aatatggaac  agtatthtaag  cgcctgtttg  540
aatctcacgg  agcgtaaacg  gttgggtggc  cagcatctga  cgcacgtgtc  gcagacgcag  600
gagcagaaca  aagagaatca  gaatcccaat  tctgatgcgc  cggatgatcag  atcaaaaact  660
tcagccaggt  acatggagct  ggtcgggtgg  ctctgggacg  cggggattac  ctcggaagaag  720
cagtggatcc  aggaggacca  ggcctcatat  atctccttca  atgcggcctc  caactcgagg  780
tccc aaatcg  cggctgcctt  ggacaatgag  ggaaagatta  tgagcctgac  taaaaccgcc  840
cccgaactacc  tgggtgggcca  gcagcccgtg  gaggacattt  ccagcaatcg  gatttataaa  900
atthttggaac  taaacgggta  cgatcccaaa  tatgcggctt  ccgtctttct  gggatgggccc  960
acgaaaaagt  tcggcgccag  gaacaccatc  tggctgtttg  ggcctgcaac  taccgggaag  1020
accaacatcg  cggaggccat  agcccacact  gtgcccttct  acgggtgctg  aaactggacc  1080
aatgagaact  ttcccttcaa  cgactgtgtc  gacaagatgg  tgatctggtg  ggaggagggg  1140
aagatgaccg  ccaaggctcg  ggagtcggcc  aaagccattc  tcggagggaag  caaggtgctg  1200
gtggaccaga  aatgcaagtc  ctgggcccag  atagaccgga  ctcccgatg  cgtcacctcc  1260
aacaccaaca  tgtgcccgt  gattgacggg  aactcaacga  ccttcgaaca  ccagcagccg  1320
ttgcaagacc  ggatgttcaa  atthgaactc  accgcgcgtc  tggatcatga  ctttgggaag  1380
gtcaccgaag  aggaagtcaa  agactttttc  cgggtgggcaa  aggatcacgt  ggttgagggtg  1440
gagcatgaat  tctacgtcaa  aaagggtgga  gccaaagaaa  gaccgcggcc  cagtgcagca  1500
gatataagtg  agcccaaacg  ggtgcgcgag  tcagttgcgc  agccatcgac  gtcagacgag  1560
gaagcttcga  tcaactacgc  agacaggtac  caaaacaaat  gttctcgta  cgtgggcatg  1620
aatctgatgc  tgtttccctg  cagacaatgc  gagagaatga  atcagaatc  aaatatctgc  1680
ttcactcacg  gacagaaaga  ctgttttag  tgctttcccg  tgtcagaatc  tcaaccggt  1740

```

-759-

tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 711  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 153 398 AGC GCG

<400> 711						
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagggt	ggtggatgag	tgctacagcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgcatacc	tggtggggcca	gcagcccggtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaaagggtg	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctc	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtoggcc	aaagccattc	tcggagggaag	cgcggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggccccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthtccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 712  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 53 216 GCG GCC

<400> 712						
acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccccgca	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240

-760-

caat	ttgaga	aggg	agagag	ctact	ttccac	atgc	cacgtgc	tcgt	ggaaac	cacc	gggggtg	300
aaat	ccatgg	tttt	ggggacg	tttct	tgagt	cagat	tcgcg	aaaa	actgat	tcag	agaatt	360
tacc	gcggga	tcga	gcccga	tttg	ccaaac	tggt	tcgcg	tcac	aaagac	cagaa	atggc	420
gccg	gagcg	ggaac	caaggt	ggtg	gatgag	tgct	acatcc	cca	attactt	gctcc	caaaa	480
accg	agcctg	agct	ccagtg	ggcg	tggact	aatat	tggaac	agtat	tttaag	cgct	gtttg	540
aatct	cacgg	agcg	taaacg	gttg	gtggcg	cagca	tctga	cgcac	gtgtc	gcag	acgcag	600
gagc	agaaca	aagaga	aatca	gaat	cccaat	tctga	tgcgc	cggt	ggccag	atca	aaaaact	660
tcag	ccaggt	acat	ggagct	ggtc	gggtgg	ctcgt	ggaca	aggg	gattac	ctcg	gagaag	720
cagt	ggatcc	aggg	aggacca	ggct	catcac	atct	ccttca	atgc	ggcctc	caact	cgcg	780
tcct	caatca	aggc	tgcctt	ggca	aatgcg	ggaa	agatta	tgag	cctgac	taaa	accgcc	840
cccg	actacc	tggt	gggcca	gcag	cccgtg	gagg	acattt	ccag	caatcg	gatt	tataaa	900
at	tttgg	aaac	taaac	cggt	ta	atgc	ggcctt	ccgt	ccttct	ggga	tgggcc	960
acg	aaaaagt	tcgg	caagag	gaac	accatc	tggt	gttttg	ggct	tgcaac	tacc	gggaag	1020
acca	acatcg	cggg	agccat	agcc	cacact	gtgc	ccttct	acgg	gtgcgt	aaact	ggacc	1080
aatg	agaact	ttcc	cttcaa	cgact	gtgtc	gaca	agatgg	tgat	ctggtg	ggag	gagggg	1140
aagat	gaccg	cca	aggtcgt	ggag	tcggcc	aaag	ccattc	tcgg	aggaag	caagt	tgcg	1200
gtgg	accaga	aatg	caagtc	ctcg	cccag	atag	accga	ctcc	cgatg	cg	cacctcc	1260
aacac	caaca	tgtg	cgccgt	gatt	gcggg	aact	caacga	cctt	cgaaca	ccag	cagccg	1320
ttgca	agacc	ggat	gttcaa	attt	gaactc	accc	gcgctc	tgga	tcatga	cttt	gggaag	1380
gtc	accaagc	agga	agtc	aa	aggtgga	gcca	agaaaa	gacc	cgcccc	gag	tgaggtg	1440
gagc	atgaat	tctac	gtcaa	aa	aggtgga	gcca	agaaaa	gacc	cgcccc	gag	tgaggtg	1500
gatata	aagt	agcc	caaacg	ggtg	cgcgag	tcag	ttgcgc	agcc	atcgac	gtcag	acgcg	1560
gaag	cttcga	caa	actacgc	agac	aggtac	gag	agaatga	atcag	aattc	aaat	atctgc	1620
aatct	gatgc	tg	tttccctg	cag	acaatgc	tgct	ttcccg	tg	tcagaatc	tca	accggt	1680
ttc	actcag	gac	agaaaga	ctg	tttagag	tgct	ttcccg	tg	tcagaatc	tca	accggt	1740
tctgt	cgta	aaa	agcgta	tcag	aaactg	tg	catatc	atc	atatac	ggg	aaaggtg	1800
ccag	acgctt	gc	actgcctg	cgat	ctggtc	aatg	tggtg	tg	gatgactg	cat	ctttgaa	1860
caata	aatga	ttta	aatcag	gtat	ggctgc	cgat	ggttat	ctt	ccagatt	gg	ctcagga	1920
cact	ctctct	ga										1932

&lt;210&gt; 713

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 22 382 GCT GCG

&lt;400&gt; 713

acgg	cggggt	ttt	acgagat	tgt	gattaag	gtccc	cagcg	acct	tgaaga	gc	atctgccc	60
ggcg	cttctg	acag	ctttgt	ga	actgggtg	gccg	agaagg	aatg	gggagtt	gcc	gccagat	120
tctg	acatgg	atct	gaatct	gatt	tgagcag	gcacc	cctga	ccgt	ggccga	ga	agctgcag	180
cgcg	actttc	tgac	ggaatg	gcgc	cggtgtg	agta	aggccc	cgg	aggccct	ttt	ctttgtg	240
caat	tttgaga	aggg	agagag	ctact	ttccac	atgc	cacgtgc	tcgt	ggaaac	cacc	gggggtg	300
aaat	ccatgg	tttt	ggggacg	tttct	tgagt	cagat	tcgcg	aaaa	actgat	tcag	agaatt	360
tacc	gcggga	tcga	gcccga	tttg	ccaaac	tggt	tcgcg	tcac	aaagac	cagaa	atggc	420
gccg	gagcg	ggaac	caaggt	ggtg	gatgag	tgct	acatcc	cca	attactt	gctcc	caaaa	480
accg	agcctg	agct	ccagtg	ggcg	tggact	aatat	tggaac	agtat	tttaag	cgct	gtttg	540
aatct	cacgg	agcg	taaacg	gttg	gtggcg	cagca	tctga	cgcac	gtgtc	gcag	acgcag	600
gagc	agaaca	aagaga	aatca	gaat	cccaat	tctga	tgcgc	cggt	gatcag	atca	aaaaact	660
tcag	ccaggt	acat	ggagct	ggtc	gggtgg	ctcgt	ggaca	aggg	gattac	ctcg	gagaag	720
cagt	ggatcc	aggg	aggacca	ggct	catcac	atct	ccttca	atgc	ggcctc	caact	cgcg	780
tcct	caatca	aggc	tgcctt	ggca	aatgcg	ggaa	agatta	tgag	cctgac	taaa	accgcc	840
cccg	actacc	tggt	gggcca	gcag	cccgtg	gagg	acattt	ccag	caatcg	gatt	tataaa	900
at	tttgg	aaac	taaac	cggt	ta	atgc	ggcctt	ccgt	ccttct	ggga	tgggcc	960
acg	aaaaagt	tcgg	caagag	gaac	accatc	tggt	gttttg	ggct	tgcaac	tacc	gggaag	1020
acca	acatcg	cggg	agccat	agcc	cacact	gtgc	ccttct	acgg	gtgcgt	aaact	ggacc	1080
aatg	agaact	ttcc	cttcaa	cgact	gtgtc	gaca	agatgg	tgat	ctggtg	ggag	gagggg	1140
aagg	cgaccg	cca	aggtcgt	ggag	tcggcc	aaag	ccattc	tcgg	aggaag	caagt	tgcg	1200
gtgg	accaga	aatg	caagtc	ctcg	cccag	atag	accga	ctcc	cgatg	cg	cacctcc	1260
aacac	caaca	tgtg	cgccgt	gatt	gcggg	aact	caacga	cctt	cgaaca	ccag	cagccg	1320

-761-

ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 714

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 231 411 GCC GCA

&lt;400&gt; 714

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactcgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgagcgaatg	gcgcctgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgctg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatcgcg	cggatgcag	atcaaaaact	660
tcagccagg	acatggagct	ggtcgggtgg	gccgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgctg	780
tcccaaatca	aggctgcctt	ggacaatgcy	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgty	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaaacgggtg	cgatccccaa	tatgcggctt	ccgtctttct	gggatggggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgtgttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccacact	gtgccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggtg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	gcagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaacccgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 715

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;



-762-

&lt;223&gt; Mutant rep DNA sequence: 59 305 GCG GCC

&lt;400&gt; 715

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaaggcgag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatgggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagg	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatatc	atctccttca	atgcggcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthtggaa	tagccgggta	cgatcccaaa	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agccccacat	gtgcctttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagacccga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgctc	tggtatcatga	ctttgggaag	1380
gtcacaagc	aggaagtcaa	agactttttc	cggtyggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgaacga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttoga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttacttcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 716

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 53 231 GCG GCC

&lt;400&gt; 716

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagcttttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccccgga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatgggaa	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccagg	acatggagct	ggtcgggtgg	gccgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatatc	atctccttca	atgcggcctc	caactcgagg	780
tcccaaatca	aggctgcctt	ggacaatg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900

-763-

atthttggaac	ttaaagggtg	cgatccccc	tatgctgctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgctg	1200
gtggaccaga	aatgcaagtc	ctcgccccag	atagaccgca	ctcccgatg	cgccacctcc	1260
aacaccaaca	tgtgcccgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcagca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgag	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgta	cggtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	atctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggct	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 717

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 258 498 GCC GCT

&lt;400&gt; 717

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcactctgcc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgccg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaaacaagg	gggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgcctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	cgccctcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tgggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaaagggtg	cgatccccc	tatgctgctt	ccgtctttct	gggatggg	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtcggcc	aaagccattc	tcggagggaag	caaggtgctg	1200
gtggaccaga	aatgcaagtc	ctcgccccag	atagaccgca	ctcccgatg	cgccacctcc	1260
aacaccaaca	tgtgcccgtg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaactc	acccgccgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	gggtgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cgctgacgca	1500
gatataagtg	agcccaaacg	gggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgag	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgta	cggtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	atctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggct	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatgggtat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

-764-

<210> 718  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 88 231 GCC GCC

<400> 718  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcattttctg acagcttttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag cgccttccac atgcacgtgc tcgtggaaac caccgggggtg 300  
 aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420  
 gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480  
 acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
 aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag 600  
 gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact 660  
 tcagccaggt acatggagct ggtcgggtgg gccgtggaca aggggattac ctcggaag 720  
 cagtggatcc aggaggacca ggccctcatac atctccttca atgcggcctc caactcgcg 780  
 tcccaaatca aggtcgctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840  
 cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
 attttggaac taaacgggta cgatccccc aaagccattc cgtctttct gggatggggc 960  
 acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggctgcaac taccgggaag 1020  
 accaaccatcg cggaggccat agcccacact gtgccttct acgggtgcgt aaactggacc 1080  
 aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
 aagatgaccg ccaaggctcg ggagtcggcc aaagccattc tcggagggaag caagggtgcgc 1200  
 gtggaccaga aatgcaagtc ctcgcccag atagaccoga ctcccgtgat cgtcacctcc 1260  
 aacaccaaca tgtgcccgt gattgacggg aactcaacga ccttcgaaca ccagcagccg 1320  
 ttgcaagacc agtagttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380  
 gtcaccaagc aggaagtcaa agactttttc cgggtggcaa aggatcacgt ggttgagggtg 1440  
 gagcatgaat tctacgtcaa aaagggtgga gccaaagaaa gaccgcgcc cagtgcagca 1500  
 gatataagtg agcccaaacg ggtgcgcgag caaaacaaat gttctcgtca cgtgggcatg 1560  
 gaagcttcga tcaactacgc agacaggtac gagagaatga atcagaattc aaatatctgc 1620  
 aatctgatgc tgtttccctg cagacaatgc ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1680  
 tttactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccggtt 1740  
 tctgtcgtca aaaagcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg 1800  
 ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa 1860  
 caataaatga tttaaatcag gtatggctgc cgatgggtat cttccagatt ggctcgagga 1920  
 cactctctct ga 1932

<210> 719  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Mutant rep DNA sequence: 101 363 GCA GCC

<400> 719  
 acggcggggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
 ggcattttctg acagcttttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
 tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
 cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
 caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccgggggtg 300  
 gcatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
 taccgcggga tcgagccgac tttgccaaac tggttcgcg tcacaaagac cagaaatggc 420  
 gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctccccaaa 480  
 acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540

-765-

aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggctcgggtg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcccgcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgaggcct	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgcgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcacagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 720

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 354 132 GCC GCC

&lt;400&gt; 720

acggcggggg	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgt	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcgggg	tcgagccgac	tttgccaaac	tgggcgcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaagg	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggctcgggtg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcccgcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccactacc	tggtggggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	cgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgcctg	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcgcgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620

-766-

aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 721

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Mutant rep DNA sequence: 10 132 GCG GCC

&lt;400&gt; 721

acggcggggt	tttacgagat	tgtgattgcg	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacggaatg	gcgcctgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttcccaaac	tgggcccggg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagg	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgccg	780
tccc aaatca	aggtgcctt	ggacaatcgc	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccaaa	tatgcggcct	ccgtctttct	gggatggggc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgccttctt	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggctcg	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccoga	ctcccgtgat	cgtaacctcc	1260
aacaccaaca	tgtgcgcccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	acccgcccgc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gaccgcggcc	cagtgcagca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctgggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 722

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; intron 630 tgc gcg

&lt;400&gt; 722

gtacaaaaac	aaatgtttctc	gtcacgtggg	catgaatctg	atgctgtttc	cctgcagaca	60
atgcgagaga	atgaatcaga	attcaaatat	ctgcttcact	cacggacaga	aagactgttt	120

-767-

agagtgccttt	cccgtgtcag	aatctcaacc	cgtttctgtc	gtcaaaaagg	cgtatcagaa	180
actgtgctac	attcatcata	tcatgggaaa	ggtgccagac	gcttgcactg	cctgcgatct	240
ggccaatgtg	gatttggatg	actgcatctt	tgaacaataa	atgattttaa	tcagggtatgg	300
cgccgatgg	ttatcttcca	g				321

<210> 723  
 <211> 321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> intron 630 tgc cgc

<400> 723						60
gtacaaaaac	aaatgttctc	gtcacgtggg	catgaatctg	atgctgtttc	cctgcagaca	120
atgcgagaga	atgaatcaga	attcaaatat	ctgcttcact	cacggacaga	aagactgttt	180
agagtgccttt	cccgtgtcag	aatctcaacc	cgtttctgtc	gtcaaaaagg	cgtatcagaa	240
actgtgctac	attcatcata	tcatgggaaa	ggtgccagac	gcttgcactg	cctgcgatct	300
ggccaatgtg	gatttggatg	actgcatctt	tgaacaataa	atgattttaa	tcagggtatgg	321
cgccgatgg	ttatcttcca	g				

<210> 724  
 <211> 321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> intron 630 tgc cct

<400> 724						60
gtacaaaaac	aaatgttctc	gtcacgtggg	catgaatctg	atgctgtttc	cctgcagaca	120
atgcgagaga	atgaatcaga	attcaaatat	ctgcttcact	cacggacaga	aagactgttt	180
agagtgccttt	cccgtgtcag	aatctcaacc	cgtttctgtc	gtcaaaaagg	cgtatcagaa	240
actgtgctac	attcatcata	tcatgggaaa	ggtgccagac	gcttgcactg	cctgcgatct	300
ggccaatgtg	gatttggatg	actgcatctt	tgaacaataa	atgattttaa	tcagggtatgg	321
ccctcgatgg	ttatcttcca	g				

<210> 725  
 <211> 321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> intron 630 tgc tca

<400> 725						60
gtacaaaaac	aaatgttctc	gtcacgtggg	catgaatctg	atgctgtttc	cctgcagaca	120
atgcgagaga	atgaatcaga	attcaaatat	ctgcttcact	cacggacaga	aagactgttt	180
agagtgccttt	cccgtgtcag	aatctcaacc	cgtttctgtc	gtcaaaaagg	cgtatcagaa	240
actgtgctac	attcatcata	tcatgggaaa	ggtgccagac	gcttgcactg	cctgcgatct	300
ggccaatgtg	gatttggatg	actgcatctt	tgaacaataa	atgattttaa	tcagggtatgg	321
ctcacgatgg	ttatcttcca	g				

<210> 726  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> mutant rep DNA sequence: 598 GAC

-768-

<400> 726  
acggcggggtggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
aatctcacgg agcgtaaacg gttgggtggc cagcatctga cgcacgtgtc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggtgatcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgagaca aggggattac ctcggaag 720  
cagtggatcc agggagacca ggcctcatal atctccttca atgcccctc caactcgcg 780  
tcccaaatca aggtgcctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840  
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
atthttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggccc 960  
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020  
accaacatcg cggaggccat agcccacact gtgcccctt acgggtgcgt aaactggacc 1080  
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg 1140  
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc 1200  
gtggaccaga aatgcaagtc ctggcccag atagaccga ccttcgaaca ccagcagccg 1260  
aacaccaaca tgtgcgccgt gattgacggg aactcaacga cgtcacctcc cgtcacctcc 1320  
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag 1380  
gtcaccaagc aggaagtcaa agactttttc cggtagggcaa aggatcacgt ggttaggtg 1440  
gagcatgaat tctacgtcaa aaagggtgga gcccaagaaa gacccgcccc cagtgacgca 1500  
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg 1560  
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg 1620  
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaatc aaatatctgc 1680  
ttcactcacg gacagaaaga ctgttttagag tgctttcccg tgtcagaatc tcaaccctg 1740  
tctgtcgtta aaaaggcgta tcagaaaactg tgctacattc atcatatcat ggacaagggt 1800  
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catcttgaa 1860  
caataaatga tttaaatcag gtatggctgc cgatggttat cttccagatt ggctcgagga 1920  
cactctctct ga 1932

&lt;210&gt; 727

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mutant rep DNA sequence: 598 AGC

<400> 727  
acggcggggtggt tttacgagat tgtgattaag gtccccagcg accttgacga gcatctgccc 60  
ggcattttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat 120  
tctgacatgg atctgaatct gattgagcag gcacccctga ccgtggccga gaagctgcag 180  
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg 240  
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg 300  
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt 360  
taccgcggga tcgagccgac tttgccaaac tggttcgcgg tcacaaagac cagaaatggc 420  
gccggaggcg ggaacaagggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa 480  
acccagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg 540  
aatctcacgg agcgtaaacg gttgggtggc cagcatctga cgcacgtgtc gcagacgcag 600  
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggtgatcag atcaaaaact 660  
tcagccaggt acatggagct ggtcgggtgg ctctgagaca aggggattac ctcggaag 720  
cagtggatcc agggagacca ggcctcatal atctccttca atgcccctc caactcgcg 780  
tcccaaatca aggtgcctt ggacaatgcg ggaagatta tgagcctgac taaaaccgcc 840  
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa 900  
atthttggaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggccc 960  
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag 1020

-769-

accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tccggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgacgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gagcaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 728

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mutant rep DNA sequence: 600 CCG

&lt;400&gt; 728

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgcagat	120
tctgacatgg	atctgaatct	gattgagcag	gcaccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcctgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggagggg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctcccaaaa	480
accagccctg	agctccagtg	ggcgtggact	aatatggaaac	agtatattaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	ggtgggtggc	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcgagaag	720
cagtggaatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tccggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cgggtgggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaaagaaa	gacccgcccc	cagtgacgca	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacagggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccggtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagccg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 729



-770-

<211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> mutant rep DNA sequence: 630 GCG

<400> 729

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccggt	gaggacattt	ccagcaatcg	gatttataaa	900
attttggaac	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccgggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgctg	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccggc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aaactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atttgaactc	accgcgcgtc	tggtatcatga	ctttgggaag	1380
gtcaccaaagc	aggaagtcaa	agactttttc	cggtygggcaa	aggatcacgt	ggttgagggtg	1440
gagcatgaat	tctacgtcaa	aaaggttgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tggtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctggttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaaggcgta	tcgaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggcgcg	cgatgggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

<210> 730  
 <211> 1932  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> mutant rep DNA sequence: 630 CGC

<400> 730

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcattctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcggtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcctgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgcg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
accagcctg	agctccagtg	ggcgtggact	aatatggaaac	agtatttaag	cgctgtttg	540
aatctcacgg	agcgtaaacg	gttgggtggc	cagcatctga	cgacgtgtc	gcagacgcag	600

-771-

gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaactc	acccgcgcgtc	tgatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agacttttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtcgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcacg	gacagaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccctgt	1740
tctgtcgtca	aaaagggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcactgcctg	cgatctggtc	aatgtggatt	tggtgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggccgc	cgatggttat	cttcagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 731

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mutant rep DNA sequence: 630 TCA

&lt;400&gt; 731

acggcgggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcatthttctg	acagctthttg	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gattgagcag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgactttc	tgacggaatg	gcgcccgtgtg	agtaaggccc	cggaggccct	tttctthttgtg	240
caattttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcgggga	tcgagccgac	tttgccaaac	tggttcgcgg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaagg	gggtgatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaaacg	gttggtggcg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggtgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatac	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgcg	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgaactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	ttaacgggta	cgatcccca	tatgcggctt	ccgtctttct	gggatgggccc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtctgtttg	ggcctgcaac	taccggggaag	1020
accaacatcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtgcggc	aaagccattc	tcggaggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgca	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aactcaacga	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaaactc	acccgcgcgtc	tgatcatga	ctttgggaag	1380
gtcaccgaagc	aggaagtcaa	agacttttttc	cgggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaaggggtgga	gccaagaaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtcgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtac	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgtttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680

-772-

ttcactcaccg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgcgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggctca	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 732

&lt;211&gt; 1932

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mutant rep DNA sequence: 630 CCT

&lt;400&gt; 732

acggcggggt	tttacgagat	tgtgattaag	gtccccagcg	accttgacga	gcatctgccc	60
ggcattttctg	acagctttgt	gaactgggtg	gccgagaagg	aatgggagtt	gccgccagat	120
tctgacatgg	atctgaatct	gatttgacag	gcacccctga	ccgtggccga	gaagctgcag	180
cgcgacttttc	tgacgggaatg	gcgccgtgtg	agtaaggccc	cggaggccct	tttctttgtg	240
caatttgaga	agggagagag	ctacttccac	atgcacgtgc	tcgtggaaac	caccgggggtg	300
aaatccatgg	ttttgggacg	tttcttgagt	cagattcgcg	aaaaactgat	tcagagaatt	360
taccgcggga	tcgagccgac	tttgccaaac	tggttcgagg	tcacaaagac	cagaaatggc	420
gccggaggcg	ggaacaaggt	ggtggatgag	tgctacatcc	ccaattactt	gctccccaaa	480
acccagcctg	agctccagtg	ggcgtggact	aatatggaac	agtatttaag	cgctgttttg	540
aatctcacgg	agcgtaaacg	gttggtggtg	cagcatctga	cgcacgtgtc	gcagacgcag	600
gagcagaaca	aagagaatca	gaatcccaat	tctgatgcgc	cggatgatcag	atcaaaaact	660
tcagccaggt	acatggagct	ggtcgggtgg	ctcgtggaca	aggggattac	ctcggagaag	720
cagtggatcc	aggaggacca	ggcctcatat	atctccttca	atgcggcctc	caactcgcgg	780
tcccaaatca	aggctgcctt	ggacaatgct	ggaaagatta	tgagcctgac	taaaaccgcc	840
cccgactacc	tggtgggcca	gcagcccgtg	gaggacattt	ccagcaatcg	gatttataaa	900
atthttggaac	taaacgggta	cgatccccc	tatgcggctt	ccgtctttct	gggatgggcc	960
acgaaaaagt	tcggcaagag	gaacaccatc	tggtgttttg	ggcctgcaac	taccgggaag	1020
accaaactcg	cggaggccat	agcccacact	gtgcccttct	acgggtgcgt	aaactggacc	1080
aatgagaact	ttcccttcaa	cgactgtgtc	gacaagatgg	tgatctgggtg	ggaggagggg	1140
aagatgaccg	ccaaggtcgt	ggagtccgcc	aaagccattc	tcggagggaag	caaggtgcgc	1200
gtggaccaga	aatgcaagtc	ctcggcccag	atagaccgga	ctcccgtgat	cgtcacctcc	1260
aacaccaaca	tgtgcgccgt	gattgacggg	aaactcaacg	ccttcgaaca	ccagcagccg	1320
ttgcaagacc	ggatgttcaa	atthtgaact	acccgccgtc	tggtatcatga	ctttgggaag	1380
gtcaccaagc	aggaagtcaa	agactttttc	cggtgggcaa	aggatcacgt	ggttgaggtg	1440
gagcatgaat	tctacgtcaa	aaagggtgga	gccaaagaaa	gacccgcccc	cagtgcgcga	1500
gatataagtg	agcccaaacg	ggtgcgcgag	tcagttgcgc	agccatcgac	gtcagacgcg	1560
gaagcttcga	tcaactacgc	agacaggtag	caaaacaaat	gttctcgtca	cgtgggcatg	1620
aatctgatgc	tgthttccctg	cagacaatgc	gagagaatga	atcagaattc	aaatatctgc	1680
ttcactcaccg	gacagaaaaga	ctgttttagag	tgctttcccg	tgtcagaatc	tcaaccgcgtt	1740
tctgtcgtca	aaaaggcgta	tcagaaactg	tgctacattc	atcatatcat	gggaaagggtg	1800
ccagacgctt	gcaactgcctg	cgatctggtc	aatgtggatt	tggatgactg	catctttgaa	1860
caataaatga	tttaaatcag	gtatggccct	cgatggttat	cttccagatt	ggctcgagga	1920
cactctctct	ga					1932

&lt;210&gt; 733

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; CMV 1 primer

&lt;400&gt; 733

tgccaagtac gccccctat

19

&lt;210&gt; 734

-773-

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> CMV 2 primer

<400> 734  
aggtcatgta ctgggcataa tgc

23

<210> 735  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> fluorescence probe VIC-Tamra

<400> 735  
tcaatgacgg taaatggccc gcct

24

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
6 March 2003 (06.03.2003)

PCT

(10) International Publication Number  
**WO 2003/018820 A3**

(51) International Patent Classification<sup>7</sup>: C12N 15/864,  
15/62, 15/35, 15/10, 7/01, 5/10, C07K 14/015, C12Q 1/70,  
A61P 15/00, 31/18, 35/00

(21) International Application Number:  
PCT/IB2002/004087

(22) International Filing Date: 16 August 2002 (16.08.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:  
60/315,382 27 August 2001 (27.08.2001) US  
10/022,390 17 December 2001 (17.12.2001) US

(71) Applicant (for all designated States except US): NAU-  
TILUS BIOTECH [FR/FR]; 1, rue Pierre Fontaine,  
F-91000 EVRY (FR).

(72) Inventors; and

(75) Inventors/Applicants (for US only): VEGA,  
Manuel [IT/FR]; 49, rue Félix Faure, F-91270 VI-  
GNEUX-SUR-SEINE (FR). DRITTANTI, Lila [IT/FR];  
49 rue Félix Faure, F-91270 VIGNEUX-SUR-SEINE  
(FR). FLAUX, Marjorie [FR/FR]; 38 rue Jules Vallès,  
F-91000 EVRY (FR).

(74) Agents: CABINET ORES et al.; 36, rue de St Péters-  
bourg, F-75008 Paris (FR).

(81) Designated States (national): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,  
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,  
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,  
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,  
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,  
SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ,  
VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM,  
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),  
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),  
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,  
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK,  
TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, ML, MR, NE, SN, TD, TG).

**Published:**

- with international search report
- with sequence listing part of description published sepa-  
rately in electronic form and available upon request from  
the International Bureau

(88) Date of publication of the international search report:  
3 June 2004

For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

WO 2003/018820 A3

(54) Title: MUTANT RECOMBINANT ADENO-ASSOCIATED VIRUSES RELATED APPLICATIONS

(57) Abstract: Mutant AAV REP proteins and their use in improving recombinant AAV production are provided.

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/IB 02/04087

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> IPC 7 C12N15/864 C12N15/62 C12N15/35 C12N15/10 C12N7/01 C12N5/10 C07K14/015 C12Q1/70 A61P15/00 A61P31/18 A61P35/00					
According to International Patent Classification (IPC) or to both national classification and IPC					
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12N C07K C12Q A61P					
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched					
Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EPO-Internal, Sequence Search, CHEM ABS Data, WPI Data, PAJ, BIOSIS, EMBASE					
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>					
Category *	Citation of document, with indication, where appropriate, of the relevant passages				Relevant to claim No.
A	WO 01/032711 A (TRUSTEES OF THE UNIVERSITY OF ;HERMONAT PAUL L (US)) 10 May 2001 (2001-05-10)  claims 11-18				1-11,13, 15-24, 39-61, 63, 65-69, 71, 73-77, 79, 81-88, 91-93
A	WO 01/025253 A (ABERNATHY CORINNE ;SAMULSKI RICHARD JUDE (US); UNIV NORTH CAROLINA) 12 April 2001 (2001-04-12) claims 6,8-11,53,54; table 1  ----- -/--				
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.					
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "&" document member of the same patent family					
Date of the actual completion of the international search			Date of mailing of the international search report		
23 September 2003			04.02.2004		
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016			Authorized officer  Lonnoy, O		

## INTERNATIONAL SEARCH REPORT

Internat  
plication No  
PCT/IB 02/04087

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	URABE MASASHI ET AL: "Charged-to-alanine scanning mutagenesis of the N-terminal half of adeno-associated virus type 2 Rep78 protein" JOURNAL OF VIROLOGY, THE AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 73, no. 4, April 1999 (1999-04), pages 2682-2693, XP002164718 ISSN: 0022-538X	
A	----- WO 99/07833 A (CELL GENESYS INC) 18 February 1999 (1999-02-18)	
A	----- WO 98/13487 A (MAXYGEN INC) 2 April 1998 (1998-04-02) -----	

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/IB 02/04087

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
**Although claims 56 and 85-87, as far as they relate to methods practiced in vivo, are directed to methods of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.**
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
**1-11, 13, 15-24, 39-61, 63, 65-69, 71, 73-77, 79, 81-88  
91-93 (all partially)**

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.



**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-11, 13, 15-24, 39-61, 63, 65-69, 71, 73-77, 79, 81-88, 91-93 (all partially)

AAV Rep mutant protein exhibiting mutation at aa 4 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; said Rep mutant protein as represented by SeqIdNo1 (F4A Rep78) or SeqIdNo.2 (F4A Rep68); nucleic acid encoding said mutant Rep protein; said nucleic acid as represented by SeqIdNo.563; AAV comprising a nucleic acid encoding said mutant Rep protein; a fusion protein comprising said mutant Rep protein; pharmaceutical composition, production method and uses thereof.

---

Inventions 2-86: claims 1-24 and 39-93 (all partially, as applicable)

As for invention 1, wherein invention 2 relates to amino and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 10 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; invention 3 relates to amino acid and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 20 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; invention 4 relates to amino acid and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 22 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype; ...; invention 86 relates to amino acid and nucleic acid sequences of an AAV Rep mutant protein that exhibits a mutation at aa 601 of AAV2 Rep78, or at the corresponding aa position in Rep of another AAV serotype.

---

Invention 87: claims 25-32 (all totally) and 1-5, 20-22, 43-56, 89-93 (all partially)

An AAV genome comprising a mutation at one or more nucleotides which encode amino acid residue 630 of AAV2 Rep78; corresponding protein, fusion protein, AAV, pharmaceutical composition, production method, and uses thereof.

---

Invention 88: claim 33 (totally)

Method of titering a virus comprising incubating a host cell with a reporter virus and the virus to be probed, measuring the output signal of the reporter virus, and comparing the titer of the reporter virus in the presence and absence of the titering virus.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

---

Invention 89: claims 34-38 (all totally)

Process for producing recombinant AAV or AAV protein having  
a predetermined property comprising characterisation and  
modification of "hit" positions, and identification of  
"lead" compounds.

---

# INTERNATIONAL SEARCH REPORT

Information on patent family members

Internati application No  
PCT/IB 02/04087

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 0132711	A	10-05-2001	AU 1436401 A WO 0132711 A2	14-05-2001 10-05-2001
WO 0125253	A	12-04-2001	AU 7739000 A WO 0125253 A2 US 6627617 B1	10-05-2001 12-04-2001 30-09-2003
WO 9907833	A	18-02-1999	US 6037177 A AU 732145 B2 AU 8825498 A CA 2300084 A1 EP 1005534 A1 JP 2001512674 T WO 9907833 A1	14-03-2000 12-04-2001 01-03-1999 18-02-1999 07-06-2000 28-08-2001 18-02-1999
WO 9813487	A	02-04-1998	AU 4503797 A AU 4597197 A CA 2266423 A1 CA 2268265 A1 EP 0964922 A1 EP 0963434 A1 JP 2001504325 T WO 9813487 A1 WO 9813485 A1 US 6319713 B1 US 6355484 B1 US 2002051976 A1	17-04-1998 17-04-1998 02-04-1998 02-04-1998 22-12-1999 15-12-1999 03-04-2001 02-04-1998 02-04-1998 20-11-2001 12-03-2002 02-05-2002